GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:00 ; Search time 106.537 Seconds
(without alignments)
1187.771 Million cell updates/sec

Title: US-10-781-181-3
Perfect score: 1540
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1540 | 100.0 | 288 | 3 | AAY93568 | Aay93568 Amino aci |
| 2 | 1430 | 92.9 | 268 | 3 | AAY93593 | Aay93593 Amino aci |
| 3 | 1430 | 92.9 | 450 | 3 | AAY93569 | Aay93569 Amino aci |
| 4 | 1430 | 92.9 | 450 | 4 | AAU08675 | Aau08675 Human pho |
| 5 | 1430 | 92.9 | 450 | 4 | AAG78915 | Aag78915 Human typ |
| 6 | 1430 | 92.9 | 450 | 8 | ADP79549 | Adp79549 Human pho |
| 7 | 1376 | 89.4 | 446 | 3 | AAY93567 | Aay93567 Amino aci |
| 8 | 1356 | 88.1 | 445 | 3 | AAY93573 | Aay93573 Amino aci |
| 9 | 1356 | 88.1 | 446 | 3 | AAY93574 | Aay93574 Amino aci |
| 10 | 1356 | 88.1 | 451 | 3 | AAY93575 | Aay93575 Amino aci |
| 11 | 1337 | 86.8 | 437 | 3 | AAY93572 | Aay93572 Amino aci |
| 12 | 1280 | 83.1 | 320 | 4 | AAB36504 | Aab36504 Human sho |
| 13 | 1280 | 83.1 | 320 | 8 | ADJ58906 | Adj58906 Human cyc |
| 14 | 1280 | 83.1 | 502 | 5 | ABB09005 | Abb09005 Human pho |
| 15 | 1280 | 83.1 | 502 | 8 | ADJ58904 | Adj58904 Human cyc |
| 16 | 1262 | 81.9 | 502 | 4 | AAB36503 | Aab36503 Human lon |
| 17 | 1259.5 | 81.8 | 413 | 3 | AAY93571 | Aay93571 Amino aci |
| 18 | 1145 | 74.4 | 391 | 4 | AAU08676 | Aau08676 Human pho |
| 19 | 980 | 63.6 | 335 | 9 | ADY50214 | Ady50214 Human PDE |
| 20 | 980 | 63.6 | 335 | 9 | ADZ46770 | Adz46770 Human PDE |
| 21 | 913 | 59.3 | 456 | 5 | AAE24530 | Aae24530 Mouse PDE |
| 22 | 907 | 58.9 | 424 | 5 | AAU79727 | Aau79727 Human cyc |
| 23 | 907 | 58.9 | 432 | 4 | AAU16967 | Aau16967 Human nov |
| 24 | 907 | 58.9 | 482 | 5 | AAE24531 | Aae24531 Human PDE |
| 25 | 907 | 58.9 | 482 | 8 | ADO40842 | Ado40842 Human pho |
| 26 | 907 | 58.9 | 482 | 8 | ADR46207 | Adr46207 Human pho |
| 27 | 907 | 58.9 | 482 | 9 | ADY18092 | Ady18092 PRO polyp |
| 28 | 907 | 58.9 | 498 | 2 | AAW00094 | Aaw00094 cAMP phos |
| 29 | 907 | 58.9 | 498 | 2 | AAY49808 | Aay49808 Human gli |
| 30 | 907 | 58.9 | 498 | 3 | AAB20619 | Aab20619 pTM22 hum |
| 31 | 907 | 58.9 | 498 | 8 | ADR66097 | Adr66097 Human pro |
| 32 | 907 | 58.9 | 498 | 8 | ADR66439 | Adr66439 Human pro |
| 33 | 906 | 58.8 | 456 | 8 | ADO21910 | Ado21910 Human cAM |
| 34 | 906 | 58.8 | 456 | 9 | ADY18172 | Ady18172 PRO polyp |
| 35 | 898 | 58.3 | 426 | 5 | AAE24528 | Aae24528 Mouse PDE |
| 36 | 892 | 57.9 | 426 | 5 | AAE24529 | Aae24529 Rat PDE7 |
| 37 | 892 | 57.9 | 428 | 5 | AAE24533 | Aae24533 Rat PDE7a |
| 38 | 891 | 57.9 | 426 | 5 | AAE24527 | Aae24527 Human PDE |
| 39 | 891 | 57.9 | 446 | 5 | AAE24532 | Aae24532 Human PDE |
| 40 | 890 | 57.8 | 441 | 8 | ABM83121 | Abm83121 Human dia |
| 41 | 890 | 57.8 | 468 | 8 | ABM83120 | Abm83120 Human dia |
| 42 | 807 | 52.4 | 424 | 5 | AAU79713 | Aau79713 Human pho |
| 43 | 788 | 51.2 | 270 | 8 | ADH61297 | Adh61297 INTSIG pr |
| 44 | 788 | 51.2 | 425 | 8 | ABM83119 | Abm83119 Human dia |
| 45 | 772 | 50.1 | 437 | 8 | ABM83118 | Abm83118 Human dia |

ALIGNMENTS

RESULT 1
AAY93568
ID AAY93568 standard; protein; 288 AA.
XX
AC AAY93568;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human phosphodiesterase enzyme.
XX
KW Phosphodiesterase; PDE-XIV; human; enzyme.
XX
OS Homo sapiens.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PF 09-NOV-1999; 99EP-00308902.
XX
PR 23-DEC-1998; 98GB-00028603.
PR 17-SEP-1999; 99GB-00022123.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Fidock M;
XX
DR WPI; 2000-433274/38.
DR N-PSDB; AAA46650.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity.
XX
PS Disclosure; Page 42-44; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens in the production of antibodies against PDE-XIV and in assays to
CC identify modulators (agonists and antagonists) of PDE-XIV expression and

CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC gene and/or expression product may be used in the preparation of a
CC composition for the treatment of a disorder associated with inappropriate
CC PDE-XIV expression and/or activity and to screen for agents that can
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC may also be used as diagnostic agents for detecting the presence of PDE-
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA))
XX
SQ Sequence 288 AA;

Query Match 100.0%; Score 1540; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.1e-162;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288
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RESULT 2
AAY93593
ID AAY93593 standard; protein; 268 AA.
XX
AC AAY93593;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human phosphodiesterase enzyme.
XX
KW Phosphodiesterase; PDE-XIV; enzyme.
XX
OS Homo sapiens.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PF 09-NOV-1999; 99EP-00308902.
XX
PR 23-DEC-1998; 98GB-00028603.
PR 17-SEP-1999; 99GB-00022123.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Fidock M;
XX
DR WPI; 2000-433274/38.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity.
XX
PS Disclosure; Page 87-88; 104pp; English.
XX

CC The present sequence represents a phosphodiesterase (PDE) enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens in the production of antibodies against PDE-XIV and in assays to
CC identify modulators (agonists and antagonists) of PDE-XIV expression and
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC gene and/or expression product may be used in the preparation of a
CC composition for the treatment of a disorder associated with inappropriate
CC PDE-XIV expression and/or activity and to screen for agents that can
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC may also be used as diagnostic agents for detecting the presence of PDE-
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA))
XX
SQ Sequence 268 AA;

Query Match 92.9%; Score 1430; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.3e-149;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
```

RESULT 3
AAY93569
ID AAY93569 standard; protein; 450 AA.
XX
AC AAY93569;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human phosphodiesterase enzyme.
XX
KW Phosphodiesterase; PDE-XIV; human; enzyme.
XX
OS Homo sapiens.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PF 09-NOV-1999; 99EP-00308902.
XX
PR 23-DEC-1998; 98GB-00028603.
PR 17-SEP-1999; 99GB-00022123.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX

PI Fidock M;
XX
DR WPI; 2000-433274/38.
DR N-PSDB; AAA46651.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity.
XX
PS Disclosure; Page 45-47; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens in the production of antibodies against PDE-XIV and in assays to
CC identify modulators (agonists and antagonists) of PDE-XIV expression and
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC gene and/or expression product may be used in the preparation of a
CC composition for the treatment of a disorder associated with inappropriate
CC PDE-XIV expression and/or activity and to screen for agents that can
CC modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC may also be used as diagnostic agents for detecting the presence of PDE-
CC XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA))
XX
SQ Sequence 450 AA;

Query Match 92.9%; Score 1430; DB 3; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.8e-149;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy 61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy 121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
||||||||||||||||||||||||||||
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 4
AAU08675
ID AAU08675 standard; protein; 450 AA.
XX
AC AAU08675;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human phosphodiesterase type 7B #1.
XX
KW Human; phosphodiesterase type 7B; cardiovascular disease; asthma;
KW allergy; inflammatory disease; immune-related disorder; cardiovascular;
KW antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200162940-A2.
XX
PD 30-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-EP001858.
XX
PR 21-FEB-2000; 2000EP-00103655.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Kluxen F, Hentsch B;
XX
DR WPI; 2001-570636/64.
DR N-PSDB; AAS13248.
XX
PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
PT diagnosing and treating, e.g. asthma, inflammation and allergies.
XX
PS Claim 1; Page 36-37; 40pp; English.
XX
CC The invention relates to a novel human Phosphodiesterase type 7B
CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC acid may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC example, The protein and nucleic acid may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P7B by expressing
CC inactive proteins or to supplement the patients own production of P7B.
CC The nucleic acids may be used to produce P7B polypeptides, by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. The nucleic acid and its complements may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acids in samples, and therefore which patients may be in
CC need of restorative therapy. The P7B polypeptides may also be used as
CC antigens in the production of antibodies against P7B and in assays to
CC identify modulators of it's expression and activity. The anti-P7B
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-P7B antibodies may also be used as diagnostic
CC agents for detecting the presence of P7B in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA)). Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include, for example
CC cardiovascular disease, asthma, allergy, inflammation, and immune-related
CC disorders. The present sequence represents a human phosphodiesterase 7B
XX
SQ Sequence 450 AA;

Query Match 92.9%; Score 1430; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.8e-149;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy 61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy 121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy 181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
||||||||||||||||||||||||||||
Db 241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268

RESULT 5

```
AAG78915
ID   AAG78915 standard; protein; 450 AA.
XX
AC   AAG78915;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Human type 7B phosphodiesterase, PDE7B.
XX
KW   Human; type 7B phosphodiesterase; PDE7B; enzyme.
XX
OS   Homo sapiens.
XX
PN   JP2001238680-A.
XX
PD   04-SEP-2001.
XX
PF   03-MAR-2000; 2000JP-00058159.
XX
PR   03-MAR-2000; 2000JP-00058159.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
DR   WPI; 2001-610057/70.
DR   N-PSDB; AAI70009.
XX
PT   New phosphodiesterase for use in the development of inhibitors of high
PT   selectivity and drugs of low side effect.
XX
PS   Claim 2; Page 12-14; 18pp; Japanese.
XX
CC   The present sequence is the protein sequence for human type 7B
CC   phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the
CC   development of inhibitors of high selectivity and drugs of low side
CC   effects
XX
SQ   Sequence 450 AA;

  Query Match             92.9%;  Score 1430;  DB 4;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-149;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 6
ADP79549
ID   ADP79549 standard; protein; 450 AA.
XX
AC   ADP79549;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human phosphodiesterase 7B nucleotide sequence.
XX
KW   Human; phosphodiesterase 7B; PDE7b; cardiovascular-gen.; CNS-Gen.;
KW   gynaecological; haemostatic; respiratory-Gen.; cytostatic; gene therapy;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2004044196-A1.
XX
PD   27-MAY-2004.
XX
PF   05-NOV-2003; 2003WO-EP012342.
XX
PR   13-NOV-2002; 2002EP-00025502.
XX
PA   (FARB ) BAYER HEALTHCARE AG.
XX
PI   Golz S,  Brueggemeier U,  Summer H;
XX
DR   WPI; 2004-440631/41.
DR   N-PSDB; ADP79548.
XX
PT   Screening for therapeutic agents, useful in treating cardiovascular,
PT   reproduction, urological, hematological, respiratory system or cancer
PT   diseases, comprises contacting a test compound with a phosphodiesterase
PT   7b.
XX
PS   Disclosure; SEQ ID NO 2; 128pp; English.
XX
CC   The present sequence is that of human phosphodiesterase 7b (PDE7b), an
CC   enzyme regulating intracellular levels of cAMP and cGMP. The invention
CC   relates to novel disease associations of PDE7b polynucleotides and
CC   polypeptides. It also relates to novel methods of screening for
CC   therapeutic agents for the treatment of cardiovascular diseases,
CC   disorders of the peripheral and central nervous system, reproduction
CC   diseases, urological diseases, haematological diseases, disorders of the
CC   respiratory system and cancer. PDE7b polynucleotides, polypeptides and
CC   regulators or modulators of PDE7b activity (e.g. an RNA molecule,
CC   antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used
CC   in the treatment or diagnosis of these diseases and disorders.
XX
SQ   Sequence 450 AA;

  Query Match             92.9%;  Score 1430;  DB 8;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-149;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 7
AAY93567
ID   AAY93567 standard; protein; 446 AA.
XX
AC   AAY93567;
XX
```

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DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a murine phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; murine; enzyme.
XX
OS   Mus sp.
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
DR   N-PSDB; AAA46649.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 39-41; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 446 AA;

  Query Match             89.4%;  Score 1376;  DB 3;  Length 446;
  Best Local Similarity   95.1%;  Pred. No. 2.7e-143;
  Matches  255;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||:|||:|:|: ||||||||:|||||||| ||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||:|||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 8
AAY93573
ID   AAY93573 standard; protein; 445 AA.
XX
AC   AAY93573;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20. .21
FT                   /label= Ser, Val, Asn, Ala
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168. .169
FT                   /label= Gly, His, Ser, Gln
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 307. .308
FT                   /label= Asp, Ala, Asn, Val
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418. .419
FT                   /label= Pro, Arg, Ser, Asn
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 423
FT   Misc-difference 427. .428
FT                   /label= Ser, Gly, Pro, Asp, His, Gln
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 430
FT                   /label= His, Leu
FT   Misc-difference 433. .434
FT                   /label= Gln, Gly, Thr, Pro, Ala
```

```
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 436. .437
FT                   /label= Ser, Glu, Thr, Leu
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 440
FT                   /note= "optionally absent"
FT   Misc-difference 443. .444
FT                   /label= Asp, Ser, Ala, Thr
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 64-66; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 445 AA;

  Query Match             88.1%;  Score 1356;  DB 3;  Length 445;
  Best Local Similarity   95.1%;  Pred. No. 4.5e-141;
  Matches  255;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| |||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 9
AAY93574
ID   AAY93574 standard; protein; 446 AA.
XX
AC   AAY93574;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 21
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 169
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 307
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 308
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 419
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 430
FT                   /label= His, Leu
FT   Misc-difference 433
FT                   /label= Gln, Gly, Thr, Pro, Ala
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FT   Misc-difference 434
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT   Misc-difference 435
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT   Misc-difference 437
FT                   /label= Ser, Glu, Thr, Leu
FT   Misc-difference 438
FT                   /label= Ser, Glu, Thr, Leu
FT   Misc-difference 441
FT                   /note= "optionally absent"
FT   Misc-difference 444
FT                   /label= Asp, Ser, Ala, Thr
FT   Misc-difference 445
FT                   /label= Asp, Ser, Ala, Thr
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 70-72; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 446 AA;

  Query Match          88.1%;  Score 1356;  DB 3;  Length 446;
  Best Local Similarity   95.1%;  Pred. No. 4.5e-141;
  Matches  255;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| |||||||||||||||| || | 
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||||| |||||||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 10
AAY93575
ID   AAY93575 standard; protein; 451 AA.
XX
AC   AAY93575;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 21
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 169
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 307
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 308
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 419
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 435
FT                   /label= His, Leu
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FT   Misc-difference 438. .440
FT                   /note= "these residues are either Gln-Gly-Pro or Pro-Ala-
FT                   Pro"
FT   Misc-difference 442. .443
FT                   /note= "these residues are either Ser-Glu or Thr-Leu"
FT   Misc-difference 446
FT                   /note= "optionally absent"
FT   Misc-difference 449. .450
FT                   /note= "these residues are either Asp-Ser or Ala-Thr"
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 75-78; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 451 AA;

  Query Match             88.1%;  Score 1356;  DB 3;  Length 451;
  Best Local Similarity   95.1%;  Pred. No. 4.6e-141;
  Matches  255;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| |||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 11
AAY93572
ID   AAY93572 standard; protein; 437 AA.
XX
AC   AAY93572;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 16
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 18
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 20
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 29
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 38
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 55
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 58
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FT   Misc-difference 113
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FT   Misc-difference 140
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FT   Misc-difference 305
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 347
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 376
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 388
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 401
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 415
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 419
FT                   /note= "any suitable peptide sequence or amino acid"
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FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 428
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 430
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 433
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 436
FT                   /note= "any suitable peptide sequence or amino acid"
XX
PN   EP1018559-A1.
XX
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PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 58-60; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 437 AA;

  Query Match             86.8%;  Score 1337;  DB 3;  Length 437;
  Best Local Similarity   95.1%;  Pred. No. 5.7e-139;
  Matches  255;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| ||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQ-XKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 59

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         60 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 119

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||  ||||||||||
Db        120 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHX-NPYHNAVHAAD 178

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 238

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        239 VLENHHWRSTIGMLRESRLLAHLPKEMT 266


RESULT 12
AAB36504
ID   AAB36504 standard; protein; 320 AA.
XX
AC   AAB36504;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human short phosphodiesterase protein SEQ ID NO:3.
XX
KW   Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
KW   cyclic nucleotide phosphodiesterase; nootropic; cardiant; hypotensive;
KW   nephrotropic; antidepressant; antiinflammatory; immunosuppressive;
KW   antiinfertility; antiasthmatic; vasotropic; gene therapy; dementia;
KW   amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
KW   glomerulonephritis; bipolar depression; bronchial asthma; salt retention;
KW   atopic disease; autoimmune encephalomyelitis; organ transplantation;
KW   nephrotic syndrome; erectile dysfunction.
XX
OS   Homo sapiens.
XX
PN   US6146876-A.
XX
PD   14-NOV-2000.
XX
PF   11-JUN-1999;   99US-00330970.
XX
PR   26-MAR-1999;   99US-00277423.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D,  Robision KE;
XX
DR   WPI; 2001-023577/03.
DR   N-PSDB; AAC87949.
XX
PT   Polynucleotide encoding novel cyclic nucleotide phosphodiesterase useful
PT   for treating disorders related with to protein e.g. dementia,
PT   hypertension, glomerulonephritis, and organ transplantation.
XX
PS   Claim 3; Fig 6; 42pp; English.
XX
CC   The present sequence represents the human short phosphodiesterase which
CC   is a cyclic nucleotide phosphodiesterase (I). (I) can have nootropic,
CC   cardiant, hypotensive, nephrotropic, antidepressant, antiinflammatory,
CC   immunosuppressive, antiinfertility, antiasthmatic and vasotropic
CC   activities, and can be used in gene therapy. (I) can be used for treating
CC   various disorders associated or mediated by (I), such as dementia,
CC   amnesia, congestive heart failure, thrombosis, pulmonary hypertension,
CC   glomerulonephritis, bipolar depression, bronchial asthma, atopic
CC   diseases, autoimmune encephalomyelitis, organ transplantation, salt
CC   retention in nephrotic syndrome and erectile dysfunction
XX
SQ   Sequence 320 AA;

  Query Match             83.1%;  Score 1280;  DB 4;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-133;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320
```

```
RESULT 13
ADJ58906
ID   ADJ58906 standard; protein; 320 AA.
XX
AC   ADJ58906;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cyclic nucleotide phosphodiesterase protein #2.
XX
KW   27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;
KW   cellular proliferation; cellular differentiation; immune disorder;
KW   cardiovascular disorder; endothelial cell disorder;
KW   haematopoietic disorder; blood vessel disorder; brain disorder; pain;
KW   metabolic disorder; liver disorder; platelet disorder; gene therapy;
KW   human; cyclic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004006016-A1.
XX
PD   08-JAN-2004.
XX
PF   11-MAR-2003; 2003US-00386414.
XX
PR   11-JUN-1999;   99US-00330970.
PR   25-OCT-1999;   99US-00426282.
PR   16-MAY-2000; 2000US-00571689.
PR   22-SEP-2000; 2000US-00668266.
PR   28-NOV-2000; 2000US-00724599.
PR   07-DEC-2000; 2000US-0254037P.
PR   10-APR-2001; 2001US-00833082.
PR   16-MAY-2001; 2001US-00860193.
PR   31-OCT-2001; 2001US-0335044P.
PR   06-DEC-2001; 2001US-00010943.
PR   29-OCT-2002; 2002US-00283023.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D,  Robison KE,  Macbeth KJ,  Carroll JM;
PI   Cook WJ,  Meyers RE,  Chun M,  Williamson MJ;
XX
DR   WPI; 2004-081738/08.
DR   N-PSDB; ADJ58905.
XX
PT   New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic
PT   acid molecules, useful for diagnosing or treating cancer, pain, or
PT   immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
PT   and liver disorders.
XX
PS   Claim 4; SEQ ID NO 6; 245pp; English.
XX
CC   The present invention relates to an isolated 27875, 22025, 27420, 17906,
CC   16319, 55092, or 10218 nucleic acid molecule. The invention is useful for
CC   diagnosing or treating cancer or aberrant cellular proliferation and/or
CC   differentiation, immune disorders, heart disorders, cardiovascular
CC   disorders including endothelial cell disorders, haematopoietic disorders,
CC   blood vessel disorders, brain disorders, pain and metabolic disorders,
CC   liver disorders and platelet disorders. The invention is also useful in
CC   gene therapy. The present sequence is human cyclic nucleotide
CC   phosphodiesterase.
XX
SQ   Sequence 320 AA;

  Query Match             83.1%;  Score 1280;  DB 8;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-133;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 14
ABB09005
ID   ABB09005 standard; protein; 502 AA.
XX
AC   ABB09005;
XX
DT   23-MAY-2002  (first entry)
XX
DE   Human phosphodiesterase-1.
XX
KW   HPDE; human phosphodiesterase; cyclic nucleotide phosphodiesterase;
KW   antiinflammatory; neuroprotective; cytostatic; antianaemic;
KW   immunosuppressive; HIV; cardiovascular disorder; mental disorder;
KW   gene therapy; transgene; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200198471-A2.
XX
PD   27-DEC-2001.
XX
PF   21-JUN-2001; 2001WO-US020140.
XX
PR   22-JUN-2000; 2000US-0213741P.
PR   14-JUL-2000; 2000US-0218234P.
PR   16-OCT-2000; 2000US-0241100P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Thornton M,  Ding L,  Patterson C,  Yao MG,  Tribouley CM,  Lal P;
PI   Hafalia AJA,  Baughn MR,  Ramkumar J,  Lu Y,  Walia NK;
XX
DR   WPI; 2002-147799/19.
DR   N-PSDB; ABA99136.
XX
PT   Novel human phosphodiesterase polypeptides and polynucleotides for
PT   diagnosing, preventing and treating eye, neurological, cardiovascular,
PT   cell proliferative and autoimmune/inflammatory disorders.
XX
PS   Claim 1; Page 97-98; 105pp; English.
XX
CC   This invention relates to isolated human phosphodiesterase polypeptides
CC   (HPDE 1-4), which are antiinflammatory, neuroprotective, cytostatic,
CC   antianaemic, immunosuppressive and anti-HIV in their action. The
CC   polypeptides are useful for screening a compound for effectiveness as an
CC   agonist or antagonist of the protein. The identified agonist, antagonist
CC   and protein are useful for treating a disease or condition associated
CC   with decreased or overexpression of functional HPDE in a patient. The
CC   proteins are useful in preparing polyclonal or monoclonal antibodies by
CC   hybridoma technology. They are also useful in the treatment and
CC   prevention of eye, neurological, cardiovascular, cell proliferative and
CC   autoimmune and inflammatory disorders, metabolic disorders and mental
CC   disorders. The polynucleotides are useful for creating humanised animals
CC   or transgenic animals to model human disease and to detect and quantify
CC   gene expression in biopsied tissues in which expression of HPDE is
```

```
CC   correlated with disease. HPDE, its fragments and antibodies specific for
CC   HPDE are useful as elements on a microarray which is useful to monitor or
CC   measure protein-protein interactions, drug-target interactions and gene
CC   expression profiles. This sequence represents HPDE-1
XX
SQ   Sequence 502 AA;

  Query Match             83.1%;  Score 1280;  DB 5;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-132;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
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Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
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Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 15
ADJ58904
ID   ADJ58904 standard; protein; 502 AA.
XX
AC   ADJ58904;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cyclic nucleotide phosphodiesterase protein #1.
XX
KW   27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;
KW   cellular proliferation; cellular differentiation; immune disorder;
KW   cardiovascular disorder; endothelial cell disorder;
KW   haematopoietic disorder; blood vessel disorder; brain disorder; pain;
KW   metabolic disorder; liver disorder; platelet disorder; gene therapy;
KW   human; cyclic; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2004006016-A1.
XX
PD   08-JAN-2004.
XX
PF   11-MAR-2003; 2003US-00386414.
XX
PR   11-JUN-1999;   99US-00330970.
PR   25-OCT-1999;   99US-00426282.
PR   16-MAY-2000; 2000US-00571689.
PR   22-SEP-2000; 2000US-00668266.
PR   28-NOV-2000; 2000US-00724599.
PR   07-DEC-2000; 2000US-0254037P.
PR   10-APR-2001; 2001US-00833082.
PR   16-MAY-2001; 2001US-00860193.
PR   31-OCT-2001; 2001US-0335044P.
PR   06-DEC-2001; 2001US-00010943.
PR   29-OCT-2002; 2002US-00283023.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D,  Robison KE,  Macbeth KJ,  Carroll JM;
PI   Cook WJ,  Meyers RE,  Chun M,  Williamson MJ;
XX
DR   WPI; 2004-081738/08.
DR   N-PSDB; ADJ58903.
XX
PT   New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic
PT   acid molecules, useful for diagnosing or treating cancer, pain, or
PT   immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
PT   and liver disorders.
XX
PS   Claim 4; SEQ ID NO 4; 245pp; English.
XX
CC   The present invention relates to an isolated 27875, 22025, 27420, 17906,
CC   16319, 55092, or 10218 nucleic acid molecule. The invention is useful for
CC   diagnosing or treating cancer or aberrant cellular proliferation and/or
CC   differentiation, immune disorders, heart disorders, cardiovascular
CC   disorders including endothelial cell disorders, haematopoietic disorders,
CC   blood vessel disorders, brain disorders, pain and metabolic disorders,
CC   liver disorders and platelet disorders. The invention is also useful in
CC   gene therapy. The present sequence is human cyclic nucleotide
CC   phosphodiesterase.
XX
SQ   Sequence 502 AA;

  Query Match             83.1%;  Score 1280;  DB 8;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-132;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


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Job time : 109.537 secs
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:57:15 ; Search time 19.9024 Seconds
(without alignments)
1392.313 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1430 | 92.9 | 450 | 2 | JC7266 | 3',5'-cyclic-nucle |
| 2 | 907 | 58.9 | 498 | 2 | A47286 | 3',5'-cyclic-AMP p |
| 3 | 331.5 | 21.5 | 584 | 2 | B53109 | 3',5'-cyclic-nucle |
| 4 | 331.5 | 21.5 | 672 | 2 | I61259 | 3',5'-cyclic-nucle |
| 5 | 330.5 | 21.5 | 673 | 2 | I61358 | 3',5'-cyclic-nucle |
| 6 | 320.5 | 20.8 | 886 | 2 | A54442 | 3',5'-cyclic-nucle |
| 7 | 317.5 | 20.6 | 562 | 2 | I59143 | cAMP phosphodieste |
| 8 | 317.5 | 20.6 | 564 | 2 | A40949 | cyclic-AMP phospho |
| 9 | 316.5 | 20.6 | 610 | 2 | I67946 | 3',5'-cyclic-nucle |
| 10 | 316.5 | 20.6 | 844 | 2 | I53865 | phosphodiesterase |
| 11 | 314.5 | 20.4 | 564 | 2 | JC1519 | 3',5'-cyclic-nucle |
| 12 | 314.5 | 20.4 | 736 | 2 | I61354 | phosphodiesterase |
| 13 | 305 | 19.8 | 712 | 2 | S71626 | 3',5'-cyclic-nucle |
| 14 | 301.5 | 19.6 | 323 | 2 | S55348 | 3',5'-cyclic-nucle |
| 15 | 296.5 | 19.3 | 534 | 1 | A44162 | 3',5'-cyclic-nucle |
| 16 | 296.5 | 19.3 | 535 | 1 | A46378 | 3',5'-cyclic-nucle |
| 17 | 295.5 | 19.2 | 535 | 1 | A44161 | 3',5'-cyclic-nucle |
| 18 | 295 | 19.2 | 536 | 2 | I67945 | 3',5'-cyclic-nucle |
| 19 | 291 | 18.9 | 519 | 2 | T14783 | hypothetical prote |
| 20 | 285 | 18.5 | 713 | 2 | JW0088 | 3',5'-cyclic-nucle |
| 21 | 282.5 | 18.3 | 536 | 1 | JC6129 | 3',5'-cyclic-nucle |
| 22 | 281 | 18.2 | 549 | 2 | T16769 | hypothetical prote |
| 23 | 279 | 18.1 | 664 | 2 | T24459 | hypothetical prote |
| 24 | 278 | 18.1 | 530 | 1 | A45334 | 3',5'-cyclic-nucle |
| 25 | 269.5 | 17.5 | 659 | 2 | JE0293 | 3',5'-cyclic-nucle |
| 26 | 269.5 | 17.5 | 885 | 2 | JC7898 | 3',5'-cyclic nucle |
| 27 | 268 | 17.4 | 777 | 2 | S65543 | 3',5'-cyclic-nucle |
| 28 | 263 | 17.1 | 768 | 2 | T10796 | 3',5'-cyclic-nucle |
| 29 | 258 | 16.8 | 491 | 2 | A40283 | 3',5'-cyclic-nucle |
| 30 | 246 | 16.0 | 267 | 2 | B33904 | cAMP phosphodieste |
| 31 | 228.5 | 14.8 | 1054 | 2 | T30901 | cyclic nucleotide |
| 32 | 223.5 | 14.5 | 875 | 1 | A48719 | 3',5'-cyclic-GMP p |
| 33 | 223.5 | 14.5 | 875 | 1 | JW0106 | 3',5'-cyclic-GMP p |
| 34 | 216.5 | 14.1 | 259 | 2 | T20399 | hypothetical prote |
| 35 | 204 | 13.2 | 1108 | 2 | A48508 | cyclic-nucleotide |
| 36 | 198.5 | 12.9 | 1112 | 2 | S70522 | cyclic nucleotide |
| 37 | 186 | 12.1 | 928 | 1 | JC2486 | 3',5'-cyclic-nucle |
| 38 | 185 | 12.0 | 921 | 1 | A40981 | 3',5'-cyclic-nucle |
| 39 | 180.5 | 11.7 | 853 | 2 | A36617 | 3',5'-cyclic-GMP p |
| 40 | 176.5 | 11.5 | 854 | 2 | A42828 | 3',5'-cyclic-GMP p |
| 41 | 176.5 | 11.5 | 856 | 1 | A47451 | 3',5'-cyclic-GMP p |
| 42 | 176 | 11.4 | 858 | 2 | JC4520 | 3',5'-cyclic-GMP p |
| 43 | 176 | 11.4 | 1141 | 2 | A44093 | cGMP-inhibited cAM |
| 44 | 175.5 | 11.4 | 800 | 2 | S13032 | 3',5'-cyclic-GMP p |
| 45 | 175.5 | 11.4 | 856 | 2 | S30762 | 3',5'-cyclic-GMP p |

ALIGNMENTS

RESULT 1
JC7266
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human
N;Alternate names: cAMP-specific phosphodiesterase 7B
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7266
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.
Biochem. Biophys. Res. Commun. 271, 575-583, 2000
A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.
A;Reference number: JC7266
A;Accession: JC7266
A;Molecule type: mRNA
A;Residues: 1-450 <SAS>
A;Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040
A;Experimental source: caudate nucleus
C;Genetics:
A;Gene: pde7B
A;Map position: 6q23-24
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase

Query Match 92.9%; Score 1430; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.2e-121;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
```

RESULT 2
A47286
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000

C;Accession: A47286
R;Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers
J. Biol. Chem. 268, 12925-12932, 1993
A;Title: Isolation and characterization of a previously undetected human cAMP phosphodie
A;Reference number: A47286; MUID:93286141; PMID:8389765
A;Accession: A47286
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-498 <MIC>
A;Cross-references: UNIPARC:UPI00001440E6; GB:L12052; NID:g179892; PID:g179893
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 58.9%; Score 907; DB 2; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.1e-73;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

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Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:|||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||||  :||  ||      |::||:|| |||: || ||| |:||||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:||||||||||||||||||||||||
Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:||||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKE 266
              ||| :|:|||| | :||| |
Db        302 WRSAVGLLRESGLFSHLPLE 321
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RESULT 3
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B53109; A34414; C33904; I67944
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: B53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <MON>
A;Cross-references: UNIPROT:P14270; UNIPARC:UPI000002A6E1; GB:U01280
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A;Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormon
A;Reference number: A34414; MUID:90046763; PMID:2554303
A;Accession: A34414
A;Molecule type: mRNA
A;Residues: 1-584 <SWI>
A;Cross-references: UNIPARC:UPI000002A6E1; GB:U09455; GB:M25349; NID:g517501; PIDN:AAA20
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: C33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 214-480 <SW2>
A;Cross-references: UNIPARC:UPI00001759B1; GB:M25349
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67944
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'EFPGES',34-421,'E',423-584 <RES>
A;Cross-references: UNIPARC:UPI00001759B2; GB:L27060; NID:g436009; PID:g436010
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative initiators; alternative splicing; cAMP binding; phosphoric diest
F;237-465/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 21.5%; Score 331.5; DB 2; Length 584;
Best Local Similarity 37.8%; Pred. No. 7.9e-22;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

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Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        130 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 186

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        187 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 245

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        246 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 305

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        306 VLENHHLAVGFKLLQE 321
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RESULT 4
I61259
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form PI
N;Alternate names: cyclic-AMP phosphodiesterase
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, sp
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000
C;Accession: I61259; A53678; I67943
R;Sette, C.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 18271-18274, 1994
A;Title: The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins differentiall
A;Reference number: A53678; MUID:94308045; PMID:8034568
A;Accession: I61259
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-672 <RES>
A;Cross-references: UNIPARC:UPI00001759B7; EMBL:U09457; NID:g517418; PID:g517419
A;Accession: A53678
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 167-672 <RE2>
A;Cross-references: UNIPARC:UPI00001707C8; EMBL:U09456; NID:g517416; PIDN:AAA20393.1; PID
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67943
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'N',96-625,'Y',627-672 <RE3>
A;Cross-references: UNIPARC:UPI0000170BF4; GB:L27059; NID:g436007; PIDN:AAA56857.1; PID:g
C;Genetics:
A;Gene: PDE3/IVd gene
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 21.5%; Score 331.5; DB 2; Length 672;
Best Local Similarity 37.8%; Pred. No. 9.5e-22;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

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Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db         218 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy         241 VLENHHWRSTIGMLRE 256
               ||||||      :|:|
Db         394 VLENHHLAVGFKLLQE 409


RESULT 5
I61358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human
N;Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: I61358; I38416
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61358
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-673 <RES>
A;Cross-references: UNIPARC:UPI0000050EB5; GB:L20970; NID:g347129; PIDN:AAA03592.1; PID:
R;Baecker, P.A.; Obernolte, R.; Bach, C.; Yee, C.; Shelton, E.R.
Gene 138, 253-256, 1994
A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiest
A;Reference number: I38416; MUID:94171048; PMID:8125310
A;Accession: I38416
A;Molecule type: mRNA
A;Residues: 70-507,'P',509-673 <RE2>
A;Cross-references: UNIPARC:UPI000016A067; EMBL:U02882; NID:g433346; PIDN:AAC13745.1; PI
C;Genetics:
A;Gene: GDB:PDE4D; DPDE3
A;Cross-references: GDB:132541; OMIM:600129
A;Map position: 5q12-5q12
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

  Query Match             21.5%;  Score 330.5;  DB 2;  Length 673;
  Best Local Similarity   37.8%;  Pred. No. 1.2e-21;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db         218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy         241 VLENHHWRSTIGMLRE 256
               ||||||      :|:|
Db         394 VLENHHLAVGFKLLQE 409


RESULT 6
A54442
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice f
N;Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A54442; S55788; A36317; S55787
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: A54442
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-886 <RES>
A;Cross-references: UNIPROT:P27815; UNIPARC:UPI0000047003; GB:L20965; NID:g347119; PIDN:
R;Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.
Cell. Signal. 6, 793-812, 1994
A;Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a h
A;Reference number: S55788; MUID:95194817; PMID:7888306
A;Accession: S55788
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-735,'E',737-886 <SUL>
A;Cross-references: UNIPARC:UPI000002A6CE; EMBL:U18087; NID:g604374; PIDN:AAC50458.1; PI
A;Note: 736-Ala was also found
R;Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Davi
Mol. Cell. Biol. 10, 2678-2686, 1990
A;Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic A
A;Reference number: A36317; MUID:90258854; PMID:2160582
A;Accession: A36317
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-516,'Y',518-722,'R',724-726,'R',728-735,'E',737-788,'E',790-
A;Cross-references: UNIPARC:UPI000017C062; GB:M37744
C;Genetics:
A;Gene: GDB:PDE4A; DPDE2
A;Cross-references: GDB:138776; OMIM:600126
A;Map position: 19p13.1-19q12
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.8%;  Score 320.5;  DB 2;  Length 886;
  Best Local Similarity   35.1%;  Pred. No. 1.3e-20;
  Matches   66;  Conservative   38;  Mismatches   81;  Indels    3;  Gaps    1;

Qy          69 VKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNG 128
               : ::   ::  |:: |    ||:  :    |: | |    |:|   |  :||      |
Db         332 MSQITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQELENLNK---WGLNIFCVSDYAGG 388

Qy         129 NSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCY 188
                 ||  ::  :|    |:  |:: : |:  ::: ::: ||:   |||::||||| |: |
Db         389 RSLTCIMYMIFQERDLLKKFRIPVDTMVTYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 448

Qy         189 LKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWR 248
               |  | | :  | |:|:  | ||| |||||||||:  ||| ||  || :| : |||||||
Db         449 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 508

Qy         249 STIGMLRE 256
                 :|:|
Db         509 VGFKLLQE 516


RESULT 7
I59143
cAMP phosphodiesterase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59143
R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A;Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAM
A;Reference number: I59143; MUID:89264471; PMID:2542941
A;Accession: I59143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-562 <RES>
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A;Cross-references: UNIPROT:P14646; UNIPARC:UPI00001440E1; GB:J04563; NID:g203967; PIDN:
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.6%;  Score 317.5;  DB 2;  Length 562;
  Best Local Similarity   34.1%;  Pred. No. 1.4e-20;
  Matches   72;  Conservative   43;  Mismatches   87;  Indels    9;  Gaps    3;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |    | :  ::  :||:| :    |:|   | :||
Db        124 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 180

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                ::   |  ::  :|    |:  ||:   |   ::: ::: |||   |||::|||||
Db        181 VAGYSHNRPLTCIMYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADV 240

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
              |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        241 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 300

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTGT 270
              |||||      :|:|    :  :| |:   |
Db        301 LENHHLAVGFKLLQEEHCDIFQNLTKKQRQT 331


RESULT 8
A40949
cyclic-AMP phosphodiesterase (EC 3.1.4.-) - rat
N;Alternate names: PDE4/IVb long form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jul-2004
C;Accession: A40949; D33904; A53109; I67942
R;Swinnen, J.V.; Tsikalas, K.E.; Conti, M.
J. Biol. Chem. 266, 18370-18377, 1991
A;Title: Properties and hormonal regulation of two structurally related cAMP phosphodies
A;Reference number: A40949; MUID:92011578; PMID:1655746
A;Accession: A40949
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <SWI>
A;Cross-references: UNIPROT:P14646; UNIPARC:UPI000002A6D9; GB:M25350
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: D33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 210-476 <SW2>
A;Cross-references: UNIPARC:UPI00001759B3; GB:M25350
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: A53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358,'S',360-564 <MON>
A;Cross-references: UNIPARC:UPI0000170820; GB:U01291; NID:g409826; PIDN:AAA18926.1; PID:
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: UNIPARC:UPI000002A6D9; GB:L27058; NID:g950096; PIDN:AAA74478.1; PID:
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.6%;  Score 317.5;  DB 2;  Length 564;
  Best Local Similarity   34.1%;  Pred. No. 1.4e-20;
  Matches   72;  Conservative   43;  Mismatches   87;  Indels    9;  Gaps    3;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |    | :  ::  :||:| :    |:|   | :||
Db        126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 182

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                ::   |  ::  :|    |:  ||:   |   ::: ::: |||   |||::|||||
Db        183 VAGYSHNRPLTCIMYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADV 242

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
              |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        243 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 302

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTGT 270
              |||||      :|:|    :  :| |:   |
Db        303 LENHHLAVGFKLLQEEHCDIFQNLTKKQRQT 333


RESULT 9
I67946
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N;Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67946; A32558; B32558; C32558
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67946
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-610 <RES>
A;Cross-references: UNIPROT:P54748; UNIPARC:UPI000002A6D4; GB:L27062; NID:g436013; PIDN:
R;Davis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A;Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+) ge
A;Reference number: A32558; MUID:89264472; PMID:2542942
A;Accession: A32558
A;Molecule type: mRNA
A;Residues: 1-598,'T',600-610 <DAV>
A;Cross-references: UNIPARC:UPI0000170937; GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:g
A;Accession: B32558
A;Molecule type: mRNA
A;Residues: 85-120,154-598,'T',600-610 <DA2>
A;Cross-references: UNIPARC:UPI0000170939; GB:M26716; GB:M26717; GB:J04554; NID:g203986;
A;Note: splice form RD2
A;Accession: C32558
A;Molecule type: mRNA
A;Residues: 26-598,'T',600-610 <DA3>
A;Cross-references: UNIPARC:UPI0000170938; GB:M26716; NID:g203984; PIDN:AAA41101.1; PID:g
A;Note: splice form RD3
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;14-20/Region: responsible for membrane association
F;26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pre
F;85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #st
F;184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.6%;  Score 316.5;  DB 2;  Length 610;
  Best Local Similarity   33.2%;  Pred. No. 1.9e-20;
  Matches   71;  Conservative   32;  Mismatches   86;  Indels   25;  Gaps    2;

Qy         43 RGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYL 102
              | | |      |    ::| : |                          :|:  :    || |
Db         80 RQSQPMSQITGLKKLVHTGSLNTN----------------------VPRFGVKTDQEDLL 117

Qy        103 GQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMV 162
                |   |||   |  :||       | ||  ::  :|    |:  | : : |:  ::: :
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Db        118 AQELENLSK---WGLNIFCVSEYAGGRSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTL 174

Qy        163 QEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQ 222
              :: ||:   |||::||||| |: |  |  | | :  | |:|:  | ||| ||||||||:
Db        175 EDHYHADVAYHNSLHAADVLQSTHVLLATPALDAVFTDLEILAALFAAAIHDVDHPGVSN 234

Qy        223 PFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRE 256
               ||| ||  || :| : |||||||      :|:|
Db        235 QFLINTNSELALMYNDESVLENHHLAVGFKLLQE 268


RESULT 10
I53865
phosphodiesterase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I53865
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I53865
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-844 <RES>
A;Cross-references: UNIPROT:P54748; UNIPARC:UPI0000127BF5; GB:L27057; NID:g3334904; PIDN
F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.6%;  Score 316.5;  DB 2;  Length 844;
  Best Local Similarity   33.2%;  Pred. No. 2.9e-20;
  Matches   71;  Conservative   32;  Mismatches   86;  Indels   25;  Gaps    2;

Qy         43 RGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYL 102
              | | |       |    ::| : |                          :|:  :    || |
Db        314 RQSQPMSQITGLKKLVHTGSLNTN----------------------VPRFGVKTDQEDLL 351

Qy        103 GQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMV 162
              |    |||   |  :||       | ||  ::  :|    |:  | : : |:  ::: :
Db        352 AQELENLSK---WGLNIFCVSEYAGGRSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTL 408

Qy        163 QEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQ 222
              :: ||:   |||::||||| |: |  |  | | :  | |:|:  | ||| ||||||||:
Db        409 EDHYHADVAYHNSLHAADVLQSTHVLLATPALDAVFTDLEILAALFAAAIHDVDHPGVSN 468

Qy        223 PFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRE 256
               ||| ||  || :| : |||||||      :|:|
Db        469 QFLINTNSELALMYNDESVLENHHLAVGFKLLQE 502


RESULT 11
JC1519
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBP106) -
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JC1519; A45500; I61359
R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, K
Gene 129, 239-247, 1993
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a
A;Reference number: JC1519; MUID:93314968; PMID:8392015
A;Accession: JC1519
A;Molecule type: mRNA
A;Residues: 1-564 <OBE>
A;Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014C5AB; GB:L12686
A;Experimental source: lymphocyte
A;Note: only partial nucleotide sequence is given
R;McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.
J. Biol. Chem. 268, 6470-6476, 1993
A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.
f mRNA.
A;Reference number: A45500; MUID:93203241; PMID:8384210
A;Accession: A45500
A;Molecule type: mRNA
A;Residues: 1-564 <MCL>
A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:g292387; PIDN:AAA36426.1; PID:g
A;Experimental source: frontal cortex
A;Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBIP:127930)
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61359
A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: UNIPARC:UPI000014C5AB; GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:g
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.4%;  Score 314.5;  DB 2;  Length 564;
  Best Local Similarity   33.6%;  Pred. No. 2.6e-20;
  Matches   71;  Conservative   44;  Mismatches   87;  Indels    9;  Gaps    3;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |     | :  ::  :||:| :    |:|   |  :||
Db        126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 182

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||
Db        183 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 242

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
               |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        243 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 302

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTGT 270
              |||||      :|:|    :  :| |:   |
Db        303 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQT 333


RESULT 12
I61354
phosphodiesterase - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I61354
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61354
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-736 <RES>
A;Cross-references: UNIPROT:Q07343; UNIPARC:UPI0000127BF6; GB:L20966; NID:g347121; PIDN:A
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             20.4%;  Score 314.5;  DB 2;  Length 736;
  Best Local Similarity   33.6%;  Pred. No. 3.6e-20;
  Matches   71;  Conservative   44;  Mismatches   87;  Indels    9;  Gaps    3;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |     | :  ::  :||:| :    |:|   |  :||
Db        298 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 354

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||
Db        355 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 414

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
               |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        415 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 474

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTGT 270
              |||||      :|:|    :  :| |:   |
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```
Db        475 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQT 505


RESULT 13
S71626
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71626; I61356
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.
FEBS Lett. 358, 305-310, 1995
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific p
A;Reference number: S71626; MUID:95145731; PMID:7843419
A;Accession: S71626
A;Molecule type: DNA
A;Residues: 1-712 <ENG>
A;Cross-references: UNIPROT:Q08493; UNIPARC:UPI0000163B31; EMBL:Z46632; NID:g727222; PID
A;Experimental source: substantia nigra
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61356
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 462-712 <RES>
A;Cross-references: UNIPARC:UPI000016AE86; GB:L20968; NID:g347125; PIDN:AAA03591.1; PID:
C;Genetics:
A;Gene: HSPDE4C1
C;Function:
A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP
A;Pathway: cyclic nucleotide metabolism
A;Note: expressed in various tissues but not in cells of the immune system
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             19.8%;  Score 305;  DB 2;  Length 712;
  Best Local Similarity   28.5%;  Pred. No. 2.5e-19;
  Matches   76;  Conservative   44;  Mismatches  107;  Indels   40;  Gaps    5;

Qy         11 EILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLN-------STTYSG-- 61
              ::. |  |:   |:  |  :: |   |  |  :         |:||         |: ||
Db        204 KLALETLDELDWCLDQLETLQTRHSVGEMASNKFK------RILNRELTHLSETSRSGNQ 257

Qy         62 --------------EIGTKK--------KVKRLLSFQRYFHASRLLRGIIPQAPLHLLDE 99
                           |:   |          : |:        |:: |    :|:  :    |
Db        258 VSEYISRTFLDQQTEVELPKVTAEEAPQPMSRISGLHGLCHSASLSSATVPRFGVQTDQE 317

Qy        100 DYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFL 159
              : | :    |      |  |:|    ::    |  ::  :|    |:  |::   ||  :|
Db        318 EQLAKE---LEDTNKWGLDVFKVADVSGNRPLTAIIFSIFQERDLLKTFQIPADTLATYL 374

Qy        160 VMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPG 219
              :|::  ||:   |||::|||| |: |  |  | | :  | |:|:  | |:| |||||||
Db        375 LMLEGHYHANVAYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALFASAIHDVDHPG 434

Qy        220 VNQPFLIKTNHHLANLYQNMSVLENHH 246
              |:  ||| ||  :| :| : |||||||
Db        435 VSNQFLINTNSDVALMYNDASVLENHH 461


RESULT 14
S55348
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) HSPDE4A7 - human
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55348
R;Horton, Y.M.; Sullivan, M.; Houslay, M.D.
Biochem. J. 308, 683-691, 1995
A;Title: Molecular cloning of a novel splice variant of human type IV(A) (PDE-IV(A)) cyd
A;Reference number: S55348; MUID:95290008; PMID:7772058
A;Accession: S55348
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-323 <HOR>
A;Cross-references: UNIPROT:P27815; UNIPARC:UPI000002A6D0; EMBL:U18088; NID:g604376; PIDN
C;Keywords: phosphoric diester hydrolase
F;98-312/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             19.6%;  Score 301.5;  DB 2;  Length 323;
  Best Local Similarity   37.3%;  Pred. No. 1.8e-19;
  Matches   66;  Conservative   32;  Mismatches   72;  Indels    7;  Gaps    4;

Qy         83 RLLRGII--PQAPLHLLDEDYLGQARHM-LSKVGMWDFDIFLFDRLTNGNSLVTLLCHLF 139
                :||  ::  |: |  ||      |  |  :  |  :||       | ||  ::  :|
Db         10 KLLGNVLQGPE-PYRLLTS---GLRLHQELENLNKWGLNIFCVSDYAGGRSLTCIMYMIF 65

Qy        140 NTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLT 199
                  |:  |:: : |:  ::: ::: ||:   |||::|||| |: |  |  | | :  |
Db         66 QERDLLKKFRIPVDTMVTYMLTLEDHYHADVAYHNSLHAADVLQSTHVLLATPALDAVFT 125

Qy        200 PLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRE 256
               |:|:  | ||| |||||||:  ||| ||  || :| : |||||||      :|:|
Db        126 DLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLLQE 182


RESULT 15
A44162
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K spl
N;Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A44162; B40283
R;Bentley, J.K.; Kadlecek, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,
J. Biol. Chem. 267, 18676-18682, 1992
A;Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodiest
A;Reference number: A44162; MUID:92406781; PMID:1326531
A;Accession: A44162
A;Molecule type: mRNA
A;Residues: 1-534 <BEN>
A;Cross-references: UNIPROT:Q01061; UNIPARC:UPI0000127BE8; GB:M94867; NID:g162782; PIDN:A
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:113352)
R;Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.
Biochemistry 30, 7940-7947, 1991
A;Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nucl
A;Reference number: A40283; MUID:91329366; PMID:1651112
A;Accession: B40283
A;Molecule type: protein
A;Residues: 29-45,'IP',48,'R',50-52,'IS',55-85;196-215;277,'D',279,'T',281-287,'T',289-29
A;Cross-references: UNIPARC:UPI0000144B58; UNIPARC:UPI000017288B; UNIPARC:UPI000017288C;
A;Experimental source: brain
C;Comment: This enzyme is a useful target for inducing the death of leukemic cells, and t
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester hy
F;220-437/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

  Query Match             19.3%;  Score 296.5;  DB 1;  Length 534;
  Best Local Similarity   37.9%;  Pred. No. 1e-18;
  Matches   61;  Conservative   30;  Mismatches   67;  Indels    3;  Gaps    2;

Qy        109 LSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHS 168
              |  | :| ||:|  :|  : ::| |::  |   | ||  ||:  | |  ||  ::  |
Db        156 LKNVDLWCFDVFSLNRAADDHALRTIVFELLTRHNLISRFKIPTVFLMTFLDALETGYGK 215

Qy        169 -QNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIK 227
               :||||| :|||||| :||:|    :   |: ::::  : ||| || :| |    | |:
Db        216 YKNPYHNQIHAADVTQTVHCFLLRTGMVHCLSEIEVLAIIFAAAIHDYEHTGTTNSFHIQ 275

Qy        228 TNHHLANLYQNMSVLENHHWRSTIGMLR--ESRLLAHLPKE 266
              |    | || : |||||||  |   |::  |  :  :| |:
Db        276 TKSECAILYNDRSVLENHHISSVFRMMQDDEMNIFINLTKD 316
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Search completed: March 10, 2006, 20:03:02
Job time : 22.9024 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:25 ; Search time 120.195 Seconds
(without alignments)
1690.519 Million cell updates/sec

Title: US-10-781-181-3
Perfect score: 1540
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1430 | 92.9 | 450 | 1 | PDE7B_HUMAN | Q9np56 homo sapien |
| 2 | 1430 | 92.9 | 450 | 2 | Q5VWY9_HUMAN | Q5vwy9 homo sapien |
| 3 | 1376 | 89.4 | 446 | 1 | PDE7B_MOUSE | Q9qxq1 mus musculu |
| 4 | 1376 | 89.4 | 446 | 2 | Q8CBS2_MOUSE | Q8cbs2 mus musculu |
| 5 | 1367 | 88.8 | 446 | 2 | Q8VIE4_RAT | Q8vie4 rattus norv |
| 6 | 1350.5 | 87.7 | 459 | 2 | Q8VIE2_RAT | Q8vie2 rattus norv |
| 7 | 1280 | 83.1 | 586 | 2 | Q4LE81_HUMAN | Q4le81 homo sapien |
| 8 | 999.5 | 64.9 | 456 | 2 | Q4RR95_TETNG | Q4rr95 tetraodon n |
| 9 | 953 | 61.9 | 359 | 2 | Q8VIE3_RAT | Q8vie3 rattus norv |
| 10 | 914 | 59.4 | 482 | 2 | Q6P5G2_MOUSE | Q6p5g2 mus musculu |
| 11 | 913 | 59.3 | 456 | 1 | PDE7A_MOUSE | P70453 mus musculu |
| 12 | 907 | 58.9 | 424 | 2 | Q96T72_HUMAN | Q96t72 homo sapien |
| 13 | 907 | 58.9 | 482 | 1 | PDE7A_HUMAN | Q13946 homo sapien |
| 14 | 906 | 58.8 | 456 | 2 | Q5R5B5_PONPY | Q5r5b5 pongo pygma |
| 15 | 892 | 57.9 | 426 | 1 | PDE7A_RAT | O08593 rattus norv |
| 16 | 775 | 50.3 | 381 | 2 | Q505M0_XENLA | Q505m0 xenopus lae |
| 17 | 711 | 46.2 | 199 | 2 | Q4VXJ0_HUMAN | Q4vxj0 homo sapien |
| 18 | 595 | 38.6 | 324 | 2 | Q4R6T4_MACFA | Q4r6t4 macaca fasc |
| 19 | 475 | 30.8 | 305 | 2 | Q7PNP5_ANOGA | Q7pnp5 anopheles g |
| 20 | 409 | 26.6 | 162 | 2 | Q86V65_HUMAN | Q86v65 homo sapien |
| 21 | 331.5 | 21.5 | 747 | 1 | PDE4D_MOUSE | Q01063 mus musculu |
| 22 | 331.5 | 21.5 | 803 | 1 | PDE4D_RAT | P14270 rattus norv |
| 23 | 330.5 | 21.5 | 809 | 1 | PDE4D_HUMAN | Q08499 homo sapien |
| 24 | 325.5 | 21.1 | 682 | 2 | Q5XGT5_XENLA | Q5xgt5 xenopus lae |
| 25 | 320.5 | 20.8 | 563 | 2 | Q5ZKR6_CHICK | Q5zkr6 gallus gall |
| 26 | 320.5 | 20.8 | 647 | 2 | Q8IVA7_HUMAN | Q8iva7 homo sapien |
| 27 | 320.5 | 20.8 | 825 | 2 | Q9H3H2_HUMAN | Q9h3h2 homo sapien |
| 28 | 320.5 | 20.8 | 860 | 2 | Q5DM53_HUMAN | Q5dm53 homo sapien |
| 29 | 320.5 | 20.8 | 864 | 2 | Q6PMT2_HUMAN | Q6pmt2 homo sapien |
| 30 | 320.5 | 20.8 | 886 | 1 | PDE4A_HUMAN | P27815 homo sapien |
| 31 | 319.5 | 20.7 | 1051 | 2 | Q4SML2_TETNG | Q4sml2 tetraodon n |
| 32 | 318.5 | 20.7 | 721 | 2 | Q9QXI7_MOUSE | Q9qxi7 mus musculu |
| 33 | 317.5 | 20.6 | 383 | 2 | Q8BQB2_MOUSE | Q8bqb2 mus musculu |
| 34 | 317.5 | 20.6 | 503 | 2 | Q6IQY6_MOUSE | Q6iqy6 mus musculu |
| 35 | 317.5 | 20.6 | 542 | 2 | Q91VY2_MOUSE | Q91vy2 mus musculu |
| 36 | 317.5 | 20.6 | 659 | 2 | Q8VD81_RAT | Q8vd81 rattus norv |
| 37 | 317.5 | 20.6 | 721 | 1 | PDE4B_RAT | P14646 rattus norv |
| 38 | 317.5 | 20.6 | 721 | 2 | Q8VBU5_MOUSE | Q8vbu5 mus musculu |
| 39 | 317.5 | 20.6 | 722 | 2 | Q5RKL0_RAT | Q5rkl0 rattus norv |
| 40 | 317.5 | 20.6 | 736 | 2 | Q8VD82_RAT | Q8vd82 rattus norv |
| 41 | 317.5 | 20.6 | 867 | 2 | Q4RL51_TETNG | Q4rl51 tetraodon n |
| 42 | 316.5 | 20.6 | 771 | 2 | Q9EQR7_RAT | Q9eqr7 rattus norv |
| 43 | 316.5 | 20.6 | 844 | 1 | PDE4A_RAT | P54748 rattus norv |
| 44 | 314.5 | 20.4 | 518 | 2 | O43850_HUMAN | O43850 homo sapien |
| 45 | 314.5 | 20.4 | 564 | 2 | Q5T3Z8_HUMAN | Q5t3z8 homo sapien |

ALIGNMENTS

RESULT 1
PDE7B_HUMAN
ID PDE7B_HUMAN STANDARD; PRT; 450 AA.
AC Q9NP56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN Name=PDE7B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;
RA Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT cAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in the control of cAMP-mediated neural

```
CC       activity and cAMP metabolism in the brain.
CC    -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC    -!- COFACTOR: Divalent cations (By similarity).
CC    -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC    -!- PATHWAY: Cyclic nucleotide metabolism.
CC    -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed in
CC       heart, liver, skeletal muscle and pancreas.
CC    -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC    -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC    ---------------------------------------------------------------------
CC    This Swiss-Prot entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC    the European Bioinformatics Institute. There are no restrictions on its
CC    use as long as its content is in no way modified and this statement is not
CC    removed.
CC    ---------------------------------------------------------------------
DR    EMBL; AB038040; BAA96537.1; -; mRNA.
DR    EMBL; AJ251860; CAB92441.1; -; mRNA.
DR    EMBL; BC075082; AAH75082.1; -; mRNA.
DR    EMBL; BC075083; AAH75083.1; -; mRNA.
DR    PIR; JC7266; JC7266.
DR    PDB; 1LXW; Model; A=104-433.
DR    Ensembl; ENSG00000171408; Homo sapiens.
DR    HGNC; HGNC:8792; PDE7B.
DR    MIM; 604645; -.
DR    GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR    GO; GO:0007165; P:signal transduction; TAS.
DR    GO; GO:0007268; P:synaptic transmission; TAS.
DR    InterPro; IPR002073; PDEase.
DR    Pfam; PF00233; PDEase_I; 1.
DR    PRINTS; PR00387; PDIESTERASE1.
DR    PROSITE; PS00126; PDEASE_I; 1.
KW    3D-structure; cAMP; Hydrolase.
FT    REGION      172    410       Catalytic (By similarity).
SQ    SEQUENCE   450 AA;  51835 MW;  EC142BF3E28D0028 CRC64;

  Query Match            92.9%;  Score 1430;  DB 1;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-122;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 2
Q5VWY9_HUMAN
ID   Q5VWY9_HUMAN PRELIMINARY;      PRT;   450 AA.
AC   Q5VWY9;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   OTTHUMP00000017267.
GN   Name=PDE7B; ORFNames=RP11-472E5.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Thomas D.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Williams S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Cobley V.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL360178; CAH73075.1; -; Genomic_DNA.
DR   EMBL; AL138828; CAI95287.1; -; Genomic_DNA.
DR   EMBL; AL133319; CAH73332.1; -; Genomic_DNA.
DR   EMBL; AL133319; CAH73075.1; JOINED; Genomic_DNA.
DR   EMBL; AL138828; CAH73075.1; JOINED; Genomic_DNA.
DR   EMBL; AL138828; CAH73332.1; JOINED; Genomic_DNA.
DR   EMBL; AL133319; CAI95287.1; JOINED; Genomic_DNA.
DR   EMBL; AL360178; CAH73332.1; JOINED; Genomic_DNA.
DR   EMBL; AL360178; CAI95287.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000171408; Homo sapiens.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
SQ   SEQUENCE   450 AA;  51835 MW;  EC142BF3E28D0028 CRC64;

  Query Match            92.9%;  Score 1430;  DB 2;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-122;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 3
PDE7B_MOUSE
ID   PDE7B_MOUSE    STANDARD;      PRT;   446 AA.
AC   Q9QXQ1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN   Name=Pde7b;
```

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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20087273; PubMed=10618442; DOI=10.1073/pnas.97.1.472;
RA   Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT   "Cloning and characterization of PDE7B, a cAMP-specific
RT   phosphodiesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
RA   Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT   "Cloning and characterisation of the human and mouse PDE7B, a novel
RT   cAMP-specific nucleotide phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC   -!- FUNCTION: May be involved in the control of cAMP-mediated neural
CC       activity and cAMP metabolism in the brain.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF190639; AAF25195.1; -; mRNA.
DR   EMBL; AJ251859; CAB92530.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSMUSG00000019990; Mus musculus.
DR   MGI; MGI:1352752; Pde7b.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   cAMP; Hydrolase.
FT   REGION      172    410       Catalytic (By similarity).
SQ   SEQUENCE   446 AA;  51337 MW;  7C052664B693A5A8 CRC64;

  Query Match             89.4%;  Score 1376;  DB 1;  Length 446;
  Best Local Similarity   95.1%;  Pred. No. 5e-117;
  Matches  255;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||:|||:|:|: ||||||||:|||||||| |||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||:|||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 4
Q8CBS2_MOUSE
ID   Q8CBS2_MOUSE PRELIMINARY;      PRT;   446 AA.
AC   Q8CBS2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male urinary bladder cDNA, RIKEN full-length
DE   enriched library, clone:9530027O16 product:phosphodiesterase 7B, full
DE   insert sequence.
GN   Name=Pde7b;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
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RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK035385; BAC29052.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   MGI; MGI:1352752; Pde7b.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   446 AA;  51307 MW;  7C002364B396A5A8 CRC64;

  Query Match             89.4%;  Score 1376;  DB 2;  Length 446;
  Best Local Similarity   95.1%;  Pred. No. 5e-117;
  Matches  255;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||:|||:|:|: ||||||||:|||||||| ||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||:||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 5
Q8VIE4_RAT
ID   Q8VIE4_RAT  PRELIMINARY;      PRT;   446 AA.
AC   Q8VIE4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17).
GN   Name=Pde7b; Synonyms=RNPDE7B;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Sasaki T., Kotera J., Omori K.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057409; BAB79637.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSRNOG00000013436; Rattus norvegicus.
DR   RGD; 621016; Pde7b.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   446 AA;  51475 MW;  01567BDABC905D19 CRC64;

  Query Match             88.8%;  Score 1367;  DB 2;  Length 446;
  Best Local Similarity   94.0%;  Pred. No. 3.3e-116;
  Matches  252;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||:|||||:|| ||||||||:|||||||| ||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFENPEQNVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||:||||:|||||||:|| |||||||: ||||||||||||||||||||||||||||||
Db         61 GEIGSKKKVRRLLSFQRHFHESRLLRGMTPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||:|||||||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 6
Q8VIE2_RAT
ID   Q8VIE2_RAT  PRELIMINARY;      PRT;   459 AA.
AC   Q8VIE2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).
GN   Name=Pde7b; Synonyms=RNPDE7B;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skeletal muscle;
RA   Sasaki T., Kotera J., Omori K.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057411; BAB79639.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSRNOG00000013436; Rattus norvegicus.
DR   RGD; 621016; Pde7b.
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DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   459 AA;  52680 MW;  A3F26E95C7FC00A5 CRC64;

  Query Match             87.7%;  Score 1350.5;  DB 2;  Length 459;
  Best Local Similarity   89.7%;  Pred. No. 1.1e-114;
  Matches  252;  Conservative   10;  Mismatches    6;  Indels   13;  Gaps    1;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCML------------GDIRLRGQTGVRAERRGSYP 47
              |||||||||||:|||||:|| ||||||              ||:|||||||| ||||||||
Db          1 MSCLMVERCGEVLFENPEQNVKCVCMLAASSPPPLPMAGQGDVRLRGQTGVPAERRGSYP 60

Qy         48 FIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARH 107
              |||||||||:||:|||||:||||:|||||||:|| ||||||: ||||||||||||||||||
Db         61 FIDFRLLNNTTHSGEIGSKKKVRRLLSFQRHFHESRLLRGMTPQAPLHLLDEDYLGQARH 120

Qy        108 MLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYH 167
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        121 MLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYH 180

Qy        168 SQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIK 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIK 240

Qy        228 TNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
              |||||||||||||||||||||||||||||||||||||||||
Db        241 TNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 281


RESULT 7
Q4LE81_HUMAN
ID   Q4LE81_HUMAN PRELIMINARY;      PRT;   586 AA.
AC   Q4LE81;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   PDE7B variant protein (Fragment).
GN   Name=PDE7B variant protein;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,
RA   Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;
RT   "Preparation of a set of expression-ready clones of mammalian long
RT   cDNAs encoding large proteins by the ORF trap cloning method.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB209990; BAE06072.1; -; mRNA.
FT   NON_TER       1      1
SQ   SEQUENCE   586 AA;  66230 MW;  F96F4F0549A9FE8D CRC64;

  Query Match             83.1%;  Score 1280;  DB 2;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-108;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 223

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 283

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 343

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 403

Qy        268 T 268
              |
Db        404 T 404


RESULT 8
Q4RR95_TETNG
ID   Q4RR95_TETNG PRELIMINARY;      PRT;   456 AA.
AC   Q4RR95;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 14 SCAF15003, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00030267001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015003; CAG09087.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     456    456
SQ   SEQUENCE   456 AA;  52118 MW;  60B4805381D70669 CRC64;

  Query Match             64.9%;  Score 999.5;  DB 2;  Length 456;
  Best Local Similarity   67.0%;  Pred. No. 1.3e-82;
  Matches  195;  Conservative   32;  Mismatches   35;  Indels   29;  Gaps    6;

Qy          7 ERCGEILFENPDQNAKCVCML----------------GDIRL-RGQTGV-RAERRGSYP 47
              :||| :   :|:|||  | ||                  : :|  |  ||   |||||||
Db          1 QRCGAVTLTSPEQNAVQVRMLDRHVDRNRPKHLPAASIAECKLSTGHAGVLLVERRGSYP 60

Qy         48 FIDFRLLNSTTYSGEI--GTKKKVKRLLSFQRYFHASRLLRGIIPQAP--LHLLDEDYLG 103
                 || ::| |::  ||:  ||::||:| |||||| |||||||::| ||  |||||: |||
Db         61 LIDLQVLKSSSQQGEVASGTRRKVQRQLSFQRYCHASRLLRGLVPHAPLSLHLLDDGYLG 120

Qy        104 QARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQ 163
```

```
                || ||||||| |:||||||||||||||||||:||||| :||:|||:|||| ||||| |||
Db        121 QAAHMLSKVGTWNFDIFLFDRLTNGNSLVTLMCHLFNVYGLVHHFQLDMVKLHRFLGMVQ 180

Qy        164 EDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQP 223
              ||||||||||||||||||||:|||||||||   |:|||: |||:|||||||||||||||
Db        181 EDYHSQNPYHNAVHAADVTQAMYCYLKEPKLAEQLSPLDVFLGLMAAAAHDVDHPGVNQP 240

Qy        224 FLIKTNHHLANLY------QNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||| ||||:||      || ||||:||||||:|||||| ||:||| :|:
Db        241 FLIKTRHHLASLYQVHQSVQNTSVLESHHWRSTVGMLRESGLLSHLPADMS 291


RESULT 9
Q8VIE3_RAT
ID   Q8VIE3_RAT  PRELIMINARY;      PRT;   359 AA.
AC   Q8VIE3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase 7B3 (EC 3.1.4.17).
GN   Name=Pde7b; Synonyms=RNPDE7B;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Sasaki T., Kotera J., Omori K.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057410; BAB79638.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   RGD; 621016; Pde7b.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   359 AA;  41456 MW;  0FF72792737CE48A CRC64;

  Query Match             61.9%;  Score 953;  DB 2;  Length 359;
  Best Local Similarity   98.3%;  Pred. No. 1.8e-78;
  Matches  176;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         90 PQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFK 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db          3 PQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHHFK 62

Qy        150 LDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLA 209
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         63 LDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLA 122

Qy        210 AAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 181


RESULT 10
Q6P5G2_MOUSE
ID   Q6P5G2_MOUSE PRELIMINARY;      PRT;   482 AA.
AC   Q6P5G2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Pde7a protein.
GN   Name=Pde7a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062909; AAH62909.1; -; mRNA.
DR   MGI; MGI:1202402; Pde7a.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   482 AA;  55189 MW;  F8460DD84BFE7B65 CRC64;

  Query Match             59.4%;  Score 914;  DB 2;  Length 482;
  Best Local Similarity   65.8%;  Pred. No. 9.4e-75;
  Matches  171;  Conservative   36;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : |||||:|:| : |   |||||:|:|||| :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||: ||    : | :|||| |||: || ||| |:||||||||||
Db        106 RNIRRLLSFQRYLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||| | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||| :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLASSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKE 266
              ||| :|:|||| | :||| |
Db        286 WRSAVGLLRESGLFSHLPLE 305


RESULT 11
PDE7A_MOUSE
ID   PDE7A_MOUSE    STANDARD;      PRT;   456 AA.
AC   P70453; Q9ERB3;
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DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (P2A).
GN   Name=Pde7a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97098542; PubMed=8943082; DOI=10.1073/pnas.93.24.14188;
RA   Bloom T.J., Beavo J.A.;
RT   "Identification and tissue-specific expression of PDE7
RT   phosphodiesterase splice variants.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC   TISSUE=Brain, and Testis;
RX   MEDLINE=20483661; PubMed=11027622; DOI=10.1006/bbrc.2000.3613;
RA   Wang P., Wu P., Egan R.W., Billah M.M.;
RT   "Cloning, characterization, and tissue distribution of mouse
RT   phosphodiesterase 7A1.";
RL   Biochem. Biophys. Res. Commun. 276:1271-1277(2000).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=PDE7A2;
CC         IsoId=P70453-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE7A1;
CC         IsoId=P70453-2; Sequence=VSP_004594;
CC   -!- TISSUE SPECIFICITY: Widely expressed with highest levels in the
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U68171; AAB08479.1; -; mRNA.
DR   EMBL; AY007702; AAG16295.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSMUSG00000019990; Mus musculus.
DR   MGI; MGI:1202402; Pde7a.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Alternative splicing; cAMP; Hydrolase.
FT   REGION      161    425       Catalytic (By similarity).
FT   VARSPLIC      1     20       MGITLIWCLALVLIKWITSK -> MEVCYQLPVLPLDRPVP
FT                                QHVLSRRGAISFSSSSALFGCPHPRQLSQ (in isoform
FT                                2).
FT                                /FTId=VSP_004594.
FT   CONFLICT    407    407       A -> D (in Ref. 2).
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SQ   SEQUENCE   456 AA;  52442 MW;  0B826B96490D9F6E CRC64;

  Query Match            59.3%;  Score 913;  DB 1;  Length 456;
  Best Local Similarity  65.8%;  Pred. No. 1.1e-74;
  Matches  171;  Conservative   36;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |   |||||:|:|||: :| :      :
Db         20 KRRGAISYDSSDQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSA 79

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||| :||: ||    : | :||||| |||: || ||| |:||||||||||
Db         80 RNIRRLLSFQRYLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLT 139

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||| | |||||:||||||||||||||||||||||||
Db        140 NGNSLVSLTFHLFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 199

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||| :|| ||:|  |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        200 CYLKEPKLASSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHH 259

Qy        247 WRSTIGMLRESRLLAHLPKE 266
              ||| :|:|||| | :||| |
Db        260 WRSAVGLLRESGLFSHLPLE 279


RESULT 12
Q96T72_HUMAN
ID   Q96T72_HUMAN PRELIMINARY;      PRT;   424 AA.
AC   Q96T72;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21265467; PubMed=11371644; DOI=10.1073/pnas.101131098;
RA   Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;
RT   "T cell activation up-regulates cyclic nucleotide phosphodiesterases
RT   8A1 and 7A3.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).
DR   EMBL; AF332652; AAK57640.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSG00000171408; Homo sapiens.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   424 AA;  48827 MW;  A7DBF40D08A7B561 CRC64;

  Query Match            58.9%;  Score 907;  DB 2;  Length 424;
  Best Local Similarity  64.6%;  Pred. No. 3.5e-74;
  Matches  168;  Conservative   39;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:|||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||| :||  ||      |::||:|| |||: || ||| |:||||||||||
Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165
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Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:||||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKE 266
              ||| :|:|||| | :||| |
Db        286 WRSAVGLLRESGLFSHLPLE 305


RESULT 13
PDE7A_HUMAN
ID   PDE7A_HUMAN    STANDARD;      PRT;   482 AA.
AC   Q13946; O15380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (HCP1) (TM22).
GN   Name=PDE7A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM PDE7A1).
RX   MEDLINE=93286141; PubMed=8389765;
RA   Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,
RA   Riggs M., Rodgers L., Beavo J.A., Wigler M.;
RT   "Isolation and characterization of a previously undetected human cAMP
RT   phosphodiesterase by complementation of cAMP phosphodiesterase-
RT   deficient Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 268:12925-12932(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM PDE7A2).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97341143; PubMed=9195912; DOI=10.1074/jbc.272.26.16152;
RA   Han P., Zhu X., Michaeli T.;
RT   "Alternative splicing of the high affinity cAMP-specific
RT   phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";
RL   J. Biol. Chem. 272:16152-16157(1997).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SUBCELLULAR LOCATION: PDE7A1 (57 kDa) is located mostly to soluble
CC       cellular fractions. PDE7A2 (50 kDa) is located to particulate
CC       cellular fractions.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=PDE7A1;
CC         IsoId=Q13946-1; Sequence=Displayed;
CC       Name=PDE7A2;
CC         IsoId=Q13946-2; Sequence=VSP_004593;
CC   -!- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal
CC       muscle and at low levels in a variety of tissues including brain
CC       and heart. It is expressed as well in two T-cell lines. PDE7A2 is
CC       found abundantly in skeletal muscle and at low levels in heart.
CC   -!- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2
CC       are found in several fetal tissues, expression is reduced
CC       throughout development. It persists strongly only in adult
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; L12052; AAA35644.2; -; mRNA.
DR   EMBL; U67932; AAB65772.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   HGNC; HGNC:8791; PDE7A.
DR   MIM; 171885; -.
DR   GO; GO:0000267; C:cell fraction; NAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Alternative splicing; cAMP; Hydrolase; Phosphorylation.
FT   REGION      187    451       Catalytic (By similarity).
FT   COMPBIAS     28     33       Poly-Ser.
FT   MOD_RES      84     84       Phosphoserine (Potential).
FT   VARSPLIC      1     46       MEVCYQLPVLPLDRPVPQHVLSRRGAISFSSSSSALFGCPNP
FT                                RQLSQ -> MGITLIWCLALVLIKWITSK (in isoform
FT                                PDE7A2).
FT                                /FTId=VSP_004593.
SQ   SEQUENCE   482 AA;  55505 MW;  3B3C8F6E9154F88C CRC64;

  Query Match             58.9%;  Score 907;  DB 1;  Length 482;
  Best Local Similarity   64.6%;  Pred. No. 4.1e-74;
  Matches  168;  Conservative   39;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
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Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
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Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:||||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
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Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKE 266
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Db        286 WRSAVGLLRESGLFSHLPLE 305


RESULT 14
Q5R5B5_PONPY
ID   Q5R5B5_PONPY PRELIMINARY;      PRT;   456 AA.
AC   Q5R5B5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp469E1731.
GN   Name=DKFZp469E1731;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
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RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR860948; CAH93051.1; -; mRNA.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   456 AA;  52755 MW;  CB162B0BFEF074BF CRC64;

  Query Match             58.8%;  Score 906;  DB 2;  Length 456;
  Best Local Similarity   64.6%;  Pred. No. 4.7e-74;
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Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         20 KRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 79

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
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Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
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Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
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Qy        247 WRSTIGMLRESRLLAHLPKE 266
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Db        260 WRSAVGLLRESGLFSHLPLE 279


RESULT 15
PDE7A_RAT
ID   PDE7A_RAT      STANDARD;      PRT;   426 AA.
AC   O08593;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
DE   (Fragment).
GN   Name=Pde7a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98176136; PubMed=9515162;
RA   Hoffmann R., Abdel'Al S., Engels P.;
RT   "Differential distribution of rat PDE-7 mRNA in embryonic and adult
RT   rat brain.";
RL   Cell Biochem. Biophys. 28:103-113(1998).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction (By similarity).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By
CC       similarity).
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U77880; AAB51234.1; -; mRNA.
DR   HSSP; Q08499; 1MKD.
DR   RGD; 68391; Pde7a.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   cAMP; Hydrolase.
FT   REGION      131     395       Catalytic (By similarity).
FT   NON_TER       1       1
SQ   SEQUENCE   426 AA;  49274 MW;  129BDC01C9351D26 CRC64;

  Query Match             57.9%;  Score 892;  DB 1;  Length 426;
  Best Local Similarity   66.7%;  Pred. No. 8.3e-73;
  Matches  166;  Conservative   33;  Mismatches   50;  Indels    0;  Gaps    0;

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              || |  : ||||:|:| : |   |||||:|:||||: :: :      : : ::|||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
              |  :||  ||       |::||||| |||: || ||| |:||||||||||||||:|  |
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Qy        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
              ||: |||| :| |||| | |||||:||||||||||||||||||||||||||||||:
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257
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Qy        258 RLLAHLPKE 266
               | :||| |
Db        241 GLFSHLPLE 249


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Job time : 124.195 secs
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OM protein - protein search, using sw model

Run on: March 10, 2006, 20:02:25 ; Search time 26.1463 Seconds
(without alignments)
910.666 Million cell updates/sec

Title: US-10-781-181-3
Perfect score: 1540
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1280 | 83.1 | 320 | 2 | US-09-330-970-3 | Sequence 3, Appli |
| 2 | 1280 | 83.1 | 502 | 2 | US-09-330-970-1 | Sequence 1, Appli |
| 3 | 1073 | 69.7 | 390 | 2 | US-09-949-016-10020 | Sequence 10020, A |
| 4 | 907 | 58.9 | 498 | 1 | US-07-688-352C-20 | Sequence 20, Appl |
| 5 | 907 | 58.9 | 498 | 1 | US-08-474-379C-20 | Sequence 20, Appl |
| 6 | 907 | 58.9 | 498 | 2 | US-09-146-249A-20 | Sequence 20, Appl |
| 7 | 907 | 58.9 | 498 | 2 | US-08-206-188B-20 | Sequence 20, Appl |
| 8 | 331.5 | 21.5 | 517 | 2 | US-09-602-735B-4 | Sequence 4, Appli |
| 9 | 330.5 | 21.5 | 451 | 1 | US-08-474-379C-61 | Sequence 61, Appl |
| 10 | 330.5 | 21.5 | 451 | 2 | US-09-146-249A-61 | Sequence 61, Appl |
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| 13 | 330.5 | 21.5 | 673 | 1 | US-08-577-492-35 | Sequence 35, Appl |
| 14 | 330.5 | 21.5 | 673 | 1 | US-08-474-379C-63 | Sequence 63, Appl |
| 15 | 330.5 | 21.5 | 673 | 2 | US-09-146-249A-63 | Sequence 63, Appl |
| 16 | 330.5 | 21.5 | 673 | 2 | US-08-206-188B-63 | Sequence 63, Appl |
| 17 | 330.5 | 21.5 | 673 | 2 | US-09-079-630-35 | Sequence 35, Appl |
| 18 | 323 | 21.0 | 302 | 4 | PCT-US91-02714-21 | Sequence 21, Appl |
| 19 | 323 | 21.0 | 398 | 1 | US-08-474-379C-86 | Sequence 86, Appl |
| 20 | 323 | 21.0 | 638 | 1 | US-07-688-352C-22 | Sequence 22, Appl |
| 21 | 323 | 21.0 | 734 | 2 | US-09-146-249A-85 | Sequence 85, Appl |
| 22 | 323 | 21.0 | 734 | 2 | US-08-206-188B-85 | Sequence 85, Appl |
| 23 | 320.5 | 20.8 | 686 | 1 | US-08-942-521B-9 | Sequence 9, Appli |
| 24 | 320.5 | 20.8 | 885 | 1 | US-08-577-492-33 | Sequence 33, Appl |
| 25 | 320.5 | 20.8 | 885 | 2 | US-09-079-630-33 | Sequence 33, Appl |
| 26 | 320.5 | 20.8 | 886 | 1 | US-08-474-379C-65 | Sequence 65, Appl |
| 27 | 320.5 | 20.8 | 886 | 2 | US-09-146-249A-65 | Sequence 65, Appl |
| 28 | 320.5 | 20.8 | 886 | 2 | US-08-206-188B-65 | Sequence 65, Appl |
| 29 | 320.5 | 20.8 | 901 | 2 | US-09-917-254-93 | Sequence 93, Appl |
| 30 | 318.5 | 20.7 | 721 | 2 | US-09-983-754-2 | Sequence 2, Appli |
| 31 | 317.5 | 20.6 | 562 | 1 | US-07-688-352C-4 | Sequence 4, Appli |
| 32 | 317.5 | 20.6 | 562 | 1 | US-08-942-521B-8 | Sequence 8, Appli |
| 33 | 317.5 | 20.6 | 562 | 1 | US-08-474-379C-4 | Sequence 4, Appli |
| 34 | 317.5 | 20.6 | 562 | 2 | US-09-146-249A-4 | Sequence 4, Appli |
| 35 | 317.5 | 20.6 | 562 | 2 | US-08-206-188B-4 | Sequence 4, Appli |
| 36 | 317.5 | 20.6 | 562 | 4 | PCT-US91-02714-4 | Sequence 4, Appli |
| 37 | 316.5 | 20.6 | 610 | 1 | US-08-974-565C-9 | Sequence 9, Appli |
| 38 | 316.5 | 20.6 | 610 | 2 | US-09-255-748-9 | Sequence 9, Appli |
| 39 | 314.5 | 20.4 | 564 | 1 | US-08-577-492-34 | Sequence 34, Appl |
| 40 | 314.5 | 20.4 | 564 | 1 | US-08-942-521B-2 | Sequence 2, Appli |
| 41 | 314.5 | 20.4 | 564 | 1 | US-08-474-379C-59 | Sequence 59, Appl |
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ALIGNMENTS

RESULT 1
US-09-330-970-3
; Sequence 3, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phophodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-3

Query Match 83.1%; Score 1280; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.8e-140;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Qy          88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
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Qy         148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Qy         208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
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Qy         268 T 268
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Db         320 T 320
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RESULT 2
US-09-330-970-1

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; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT: White, David
;  TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
;  TITLE OF INVENTION: Phophodiesterase
;  FILE REFERENCE: 5800-28
;  CURRENT APPLICATION NUMBER: US/09/330,970
;  CURRENT FILING DATE: 1999-06-11
;  EARLIER APPLICATION NUMBER: 09/277,423
;  EARLIER FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-330-970-1

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Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
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Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
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Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
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Db        320 T 320


RESULT 3
US-09-949-016-10020
; Sequence 10020, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10020
;   LENGTH: 390
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10020

  Query Match             69.7%;  Score 1073;  DB 2;  Length 390;
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  Matches  208;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

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Qy         89 IPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHF 148
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Db         61 IPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTN---------------------- 99

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                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 -----------VMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLL 148

Qy        209 AAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 208


RESULT 4
US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/688,352C
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-688-352C-20

  Query Match             58.9%;  Score 907;  DB 1;  Length 498;
  Best Local Similarity   64.6%;  Pred. No. 1.8e-96;
  Matches  168;  Conservative   39;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121
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```
Qy          67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
               : ::|||||||| :|| ||      |::||:|| ||||: || ||| |:||||||||||
Db         122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy         127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
               ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db         182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy         187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
               |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db         242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy         247 WRSTIGMLRESRLLAHLPKE 266
               ||| :|:|||| | :||| |
Db         302 WRSAVGLLRESGLFSHLPLE 321
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RESULT 5
US-08-474-379C-20
; Sequence 20, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,379C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,188
; FILING DATE: 01-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,352
; FILING DATE: 19-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 27866/32771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-379C-20

Query Match 58.9%; Score 907; DB 1; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

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Qy           7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
               :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db          62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy          67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
               : ::|||||||| :|| ||      |::||:|| ||||: || ||| |:||||||||||
Db         122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy         127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
               ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db         182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy         187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
               |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db         242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy         247 WRSTIGMLRESRLLAHLPKE 266
               ||| :|:|||| | :||| |
Db         302 WRSAVGLLRESGLFSHLPLE 321
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RESULT 6
US-09-146-249A-20
; Sequence 20, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-146-249A-20

Query Match 58.9%; Score 907; DB 2; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

```
Qy           7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
               :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db          62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121
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Qy          67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
               : ::|||||||| :|| || |::||:|| |||: || ||| |:|||||||||
Db         122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy         127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
               |||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db         182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy         187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
               |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db         242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy         247 WRSTIGMLRESRLLAHLPKE 266
               ||| :|:|||| | :||| |
Db         302 WRSAVGLLRESGLFSHLPLE 321
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RESULT 7
US-08-206-188B-20
; Sequence 20, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-188B-20

Query Match 58.9%; Score 907; DB 2; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.8e-96;
Matches 168; Conservative 39; Mismatches 53; Indels 0; Gaps 0;

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Qy           7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
               :| | | ::: || |  : ||||:|:| : |  :|||||:|:|||: :|  :      :
Db          62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy          67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
               : ::|||||||| :|| || |::||:|| |||: || ||| |:|||||||||
Db         122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy         127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
               |||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db         182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy         187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
               |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db         242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy         247 WRSTIGMLRESRLLAHLPKE 266
               ||| :|:|||| | :||| |
Db         302 WRSAVGLLRESGLFSHLPLE 321
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RESULT 8
US-09-602-735B-4
; Sequence 4, Application US/09602735B
; Patent No. 6656717
; GENERAL INFORMATION:
; APPLICANT: Xin, Xiaonan
; APPLICANT: Unterbeck, Axel
; APPLICANT: Hu, Yinghe
; TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 453260-55
; CURRENT APPLICATION NUMBER: US/09/602,735B
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/141,196
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-602-735B-4

Query Match 21.5%; Score 331.5; DB 2; Length 517;
Best Local Similarity 37.8%; Pred. No. 1.7e-29;
Matches 74; Conservative 35; Mismatches 78; Indels 9; Gaps 4;

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Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db          63 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 119

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         120 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 178

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| |||||||:  ||| ||  || :| : |
Db         179 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 238

Qy         241 VLENHHWRSTIGMLRE 256
               ||||||      :|:|
Db         239 VLENHHLAVGFKLLQE 254
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RESULT 9
US-08-474-379C-61
; Sequence 61, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois

```
;       COUNTRY:  United States of America
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/474,379C
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/511,715
;       FILING DATE:  20-APR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/206,188
;       FILING DATE:  01-MAR-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/688,352
;       FILING DATE:  19-APR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clough, David W.
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  27866/32771
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 474-6300
;       TELEFAX:  (312) 474-0448
;   INFORMATION FOR SEQ ID NO:  61:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  451 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-474-379C-61

  Query Match             21.5%;  Score 330.5;  DB 1;  Length 451;
  Best Local Similarity   37.8%;  Pred. No. 1.8e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        234 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 290

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        291 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 349

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        350 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 409

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        410 VLENHHLAVGFKLLQE 425


RESULT 10
US-09-146-249A-61
; Sequence 61, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-61

  Query Match             21.5%;  Score 330.5;  DB 2;  Length 451;
  Best Local Similarity   37.8%;  Pred. No. 1.8e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        234 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 290

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        291 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 349

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        350 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 409

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        410 VLENHHLAVGFKLLQE 425


RESULT 11
US-08-206-188B-61
; Sequence 61, Application US/08206188B
; Patent No. 6100025
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/206,188B
;      FILING DATE:  01-MAR-1994
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;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/511,715
;       FILING DATE:  20-APR-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clough, David W.
;       REGISTRATION NUMBER:  36107
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/474-6300
;       TELEFAX:  312-474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  61:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  451 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-206-188B-61

  Query Match             21.5%;  Score 330.5;  DB 2;  Length 451;
  Best Local Similarity   37.8%;  Pred. No. 1.8e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        234 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 290

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        291 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 349

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        350 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 409

Qy        241 VLENHHWRSTIGMLRE 256
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Db        410 VLENHHLAVGFKLLQE 425


RESULT 12
US-09-602-735B-2
; Sequence 2, Application US/09602735B
; Patent No. 6656717
; GENERAL INFORMATION:
;  APPLICANT: Xin, Xiaonan
;  APPLICANT:  Unterbeck, Axel
;  APPLICANT:  Hu, Yinghe
;  TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 453260-55
;  CURRENT APPLICATION NUMBER: US/09/602,735B
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: U.S. 60/141,196
;  PRIOR FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 518
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-602-735B-2

  Query Match             21.5%;  Score 330.5;  DB 2;  Length 518;
  Best Local Similarity   37.8%;  Pred. No. 2.2e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
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Db         63 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 119

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
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Db        120 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 178

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        179 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 238

Qy        241 VLENHHWRSTIGMLRE 256
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Db        239 VLENHHLAVGFKLLQE 254


RESULT 13
US-08-577-492-35
; Sequence 35, Application US/08577492
; Patent No. 5851784
;  GENERAL INFORMATION:
;    APPLICANT:  Owens, Raymond John
;    APPLICANT:  Perry, Martin John
;    APPLICANT:  Lumb, Simon Mark
;    TITLE OF INVENTION:  HUMAN PHOSPHODIESTERASE TYPE IVC, AND
;    TITLE OF INVENTION:  ITS PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/577,492
;      FILING DATE:  22-DEC-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426227.6
;      FILING DATE:  23-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9512996.1
;      FILING DATE:  26-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherry, David A.
;      REGISTRATION NUMBER:  35,099
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
US-08-577-492-35

  Query Match             21.5%;  Score 330.5;  DB 1;  Length 673;
  Best Local Similarity   37.8%;  Pred. No. 3.3e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
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Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393
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Qy        241 VLENHHWRSTIGMLRE 256
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Db        394 VLENHHLAVGFKLLQE 409


RESULT 14
US-08-474-379C-63
; Sequence 63, Application US/08474379C
; Patent No. 5977305
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  CLONING BY COMPLEMENTATION AND RELATED
;    TITLE OF INVENTION:  PROCESSES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,379C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/206,188
;      FILING DATE:  01-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/688,352
;      FILING DATE:  19-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  27866/32771
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-474-379C-63

  Query Match             21.5%;  Score 330.5;  DB 1;  Length 673;
  Best Local Similarity   37.8%;  Pred. No. 3.3e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
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Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
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Db        394 VLENHHLAVGFKLLQE 409


RESULT 15
US-09-146-249A-63
; Sequence 63, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-63

  Query Match             21.5%;  Score 330.5;  DB 2;  Length 673;
  Best Local Similarity   37.8%;  Pred. No. 3.3e-29;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||: :    || | :   |  | |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        394 VLENHHLAVGFKLLQE 409


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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:18:07 ; Search time 87.0244 Seconds
(without alignments)
1382.771 Million cell updates/sec

Title: US-10-781-181-3
Perfect score: 1540
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 2 | 1430 | 92.9 | 450 | 4 | US-10-781-181-5 | Sequence 5, Appli |
| 3 | 1430 | 92.9 | 450 | 5 | US-10-204-268A-2 | Sequence 2, Appli |
| 4 | 1376 | 89.4 | 446 | 4 | US-10-781-181-1 | Sequence 1, Appli |
| 5 | 1280 | 83.1 | 320 | 4 | US-10-386-414-6 | Sequence 6, Appli |
| 6 | 1280 | 83.1 | 502 | 4 | US-10-273-517-1 | Sequence 1, Appli |
| 7 | 1280 | 83.1 | 502 | 4 | US-10-386-414-4 | Sequence 4, Appli |
| 8 | 1280 | 83.1 | 502 | 4 | US-10-311-104-1 | Sequence 1, Appli |
| 9 | 1280 | 83.1 | 502 | 6 | US-11-048-744-1 | Sequence 1, Appli |
| 10 | 1280 | 83.1 | 502 | 6 | US-11-048-068-1 | Sequence 1, Appli |
| 11 | 1145 | 74.4 | 391 | 5 | US-10-204-268A-4 | Sequence 4, Appli |
| 12 | 980 | 63.6 | 335 | 5 | US-10-771-833-23 | Sequence 23, Appl |
| 13 | 980 | 63.6 | 335 | 5 | US-10-886-949-23 | Sequence 23, Appl |
| 14 | 907 | 58.9 | 424 | 5 | US-10-380-437-6 | Sequence 6, Appli |
| 15 | 907 | 58.9 | 424 | 5 | US-10-380-437-53 | Sequence 53, Appl |
| 16 | 907 | 58.9 | 432 | 3 | US-09-764-898-208 | Sequence 208, App |
| 17 | 898 | 58.3 | 426 | 3 | US-09-966-781A-2 | Sequence 2, Appli |
| 18 | 892 | 57.9 | 426 | 3 | US-09-966-781A-3 | Sequence 3, Appli |
| 19 | 891 | 57.9 | 426 | 3 | US-09-966-781A-1 | Sequence 1, Appli |
| 20 | 725 | 47.1 | 334 | 5 | US-10-771-833-22 | Sequence 22, Appl |
| 21 | 725 | 47.1 | 334 | 5 | US-10-886-949-22 | Sequence 22, Appl |
| 22 | 682 | 44.3 | 336 | 4 | US-10-258-746-2 | Sequence 2, Appli |
| 23 | 531 | 34.5 | 99 | 4 | US-10-781-181-16 | Sequence 16, Appl |
| 24 | 392 | 25.5 | 211 | 3 | US-09-764-898-280 | Sequence 280, App |
| 25 | 392 | 25.5 | 211 | 3 | US-09-989-442-120 | Sequence 120, App |
| 26 | 331.5 | 21.5 | 517 | 4 | US-10-682-722-4 | Sequence 4, Appli |
| 27 | 331.5 | 21.5 | 747 | 5 | US-10-492-835-8 | Sequence 8, Appli |
| 28 | 331.5 | 21.5 | 747 | 5 | US-10-492-835-15 | Sequence 15, Appl |
| 29 | 331.5 | 21.5 | 747 | 5 | US-10-492-835-27 | Sequence 27, Appl |
| 30 | 330.5 | 21.5 | 507 | 4 | US-10-076-597-49 | Sequence 49, Appl |
| 31 | 330.5 | 21.5 | 507 | 4 | US-10-067-514-10 | Sequence 10, Appl |
| 32 | 330.5 | 21.5 | 507 | 4 | US-10-419-723-10 | Sequence 10, Appl |
| 33 | 330.5 | 21.5 | 507 | 4 | US-10-255-120-10 | Sequence 10, Appl |
| 34 | 330.5 | 21.5 | 507 | 4 | US-10-755-889-304 | Sequence 304, App |
| 35 | 330.5 | 21.5 | 507 | 5 | US-10-868-397-10 | Sequence 10, Appl |
| 36 | 330.5 | 21.5 | 518 | 4 | US-10-682-722-2 | Sequence 2, Appli |
| 37 | 330.5 | 21.5 | 585 | 4 | US-10-067-514-9 | Sequence 9, Appli |
| 38 | 330.5 | 21.5 | 585 | 4 | US-10-419-723-9 | Sequence 9, Appli |
| 39 | 330.5 | 21.5 | 585 | 4 | US-10-255-120-9 | Sequence 9, Appli |
| 40 | 330.5 | 21.5 | 585 | 5 | US-10-868-397-9 | Sequence 9, Appli |
| 41 | 330.5 | 21.5 | 664 | 5 | US-10-735-973-2 | Sequence 2, Appli |
| 42 | 330.5 | 21.5 | 673 | 4 | US-10-076-597-51 | Sequence 51, Appl |
| 43 | 330.5 | 21.5 | 673 | 4 | US-10-067-514-6 | Sequence 6, Appli |
| 44 | 330.5 | 21.5 | 673 | 4 | US-10-419-723-6 | Sequence 6, Appli |
| 45 | 330.5 | 21.5 | 673 | 4 | US-10-255-120-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-10-781-181-3
; Sequence 3, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: Enzyme PDE xiv
; FILE REFERENCE: PC10315B
; CURRENT APPLICATION NUMBER: US/10/781,181
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: GB 9828603.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/471,459
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 9922123.6
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Human
US-10-781-181-3

Query Match 100.0%; Score 1540; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 3e-154;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
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Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288
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Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRLTNGNSLV 288
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RESULT 2
US-10-781-181-5
; Sequence 5, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Enzyme PDE xiv
;  FILE REFERENCE: PC10315B
;  CURRENT APPLICATION NUMBER: US/10/781,181
;  CURRENT FILING DATE:  2004-02-18
;  PRIOR APPLICATION NUMBER: GB 9828603.2
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: US 09/471,459
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: GB 9922123.6
;  PRIOR FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Human
US-10-781-181-5

  Query Match             92.9%;  Score 1430;  DB 4;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-142;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
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Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
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Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
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Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
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Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268.


RESULT 3
US-10-204-268A-2
; Sequence 2, Application US/10204268A
; Publication No. US20050058647A1
; GENERAL INFORMATION:
;  APPLICANT: KLUXEN, FRANZ-WERNER
;  APPLICANT:  HENTSCH, BERND
;  TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
;  FILE REFERENCE: MERCK-2484
;  CURRENT APPLICATION NUMBER: US/10/204,268A
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: PCT/EP01/01858
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: EP 00103655.7
;  PRIOR FILING DATE: 2000-02-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-204-268A-2

  Query Match             92.9%;  Score 1430;  DB 5;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-142;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 4
US-10-781-181-1
; Sequence 1, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Enzyme PDE xiv
;  FILE REFERENCE: PC10315B
;  CURRENT APPLICATION NUMBER: US/10/781,181
;  CURRENT FILING DATE:  2004-02-18
;  PRIOR APPLICATION NUMBER: GB 9828603.2
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: US 09/471,459
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: GB 9922123.6
;  PRIOR FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Mouse
US-10-781-181-1

  Query Match             89.4%;  Score 1376;  DB 4;  Length 446;
  Best Local Similarity   95.1%;  Pred. No. 1.3e-136;
  Matches  255;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||:|||:|:|: ||||||||:||||||| |||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||:|||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
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RESULT 5
US-10-386-414-6
; Sequence 6, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT:  Robison, Keith E.
;  APPLICANT:  White, David
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Cook, William James
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
;  TITLE OF INVENTION:  55092 AND 10218 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-021OMNIM
;  CURRENT APPLICATION NUMBER: US/10/386,414
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: 09/426,282
;  PRIOR FILING DATE: 1999-10-25
;  PRIOR APPLICATION NUMBER: 09/668,266
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/330,970
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: 09/724,599
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/860,193
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: 10/283,023
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,044
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/010,943
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 60/254,037
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: 09/833,082
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 320
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-386-414-6

  Query Match             83.1%;  Score 1280;  DB 4;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy          88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy         148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy         208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy         268 T 268
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Db         320 T 320


RESULT 6
US-10-273-517-1
; Sequence 1, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:
;  APPLICANT: THORNTON, Michael B.; DING, Li
;  APPLICANT:  ARVIZU, Chandra S.; YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.; LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.; BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; LU, Yan
;  APPLICANT:  CHAWLA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 USA
;  CURRENT APPLICATION NUMBER: US/10/273,517
;  CURRENT FILING DATE:  2002-10-18
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1
US-10-273-517-1

  Query Match             83.1%;  Score 1280;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy          88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy         148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy         208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy         268 T 268
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Db         320 T 320


RESULT 7
US-10-386-414-4
; Sequence 4, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT:  Robison, Keith E.
;  APPLICANT:  White, David
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Cook, William James
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Carroll, Joseph M.
```

```
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
;  TITLE OF INVENTION:  55092 AND 10218 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-021OMNIM
;  CURRENT APPLICATION NUMBER: US/10/386,414
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: 09/426,282
;  PRIOR FILING DATE: 1999-10-25
;  PRIOR APPLICATION NUMBER: 09/668,266
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/330,970
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: 09/724,599
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/860,193
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: 10/283,023
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,044
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/010,943
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 60/254,037
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: 09/833,082
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-386-414-4

  Query Match             83.1%;  Score 1280;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 8
US-10-311-104-1
; Sequence 1, Application US/10311104
; Publication No. US20040054138A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  DING, Li
;  APPLICANT:  ARIVZU Chandra S.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  LU, Yan
;  APPLICANT:  Chawla, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,104
;  CURRENT FILING DATE:  2002-12-12
;  PRIOR APPLICATION NUMBER: PCT/US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
US-10-311-104-1

  Query Match             83.1%;  Score 1280;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 9
US-11-048-744-1
; Sequence 1, Application US/11048744
; Publication No. US20050164275A1
; GENERAL INFORMATION:
;  APPLICANT: THORNTON, Michael B.; DING, Li
;  APPLICANT:  ARVIZU, Chandra S.; YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.; LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.; BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; LU, Yan
;  APPLICANT:  CHAWLA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 USA
;  CURRENT APPLICATION NUMBER: US/11/048,744
;  CURRENT FILING DATE:  2005-02-03
;  PRIOR APPLICATION NUMBER: US/10/273,517
;  PRIOR FILING DATE: 2002-10-18
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/20140
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;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7476201CD1
US-11-048-744-1

  Query Match            83.1%;  Score 1280;  DB 6;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 10
US-11-048-068-1
; Sequence 1, Application US/11048068
; Publication No. US20050202478A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  DING, Li
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  HAFALIA, April J. A.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  LU, Yan
;  APPLICANT:  WALIA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 PCT
;  CURRENT APPLICATION NUMBER: US/11/048,068
;  CURRENT FILING DATE:  2005-02-02
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7476201CD1
US-11-048-068-1

  Query Match            83.1%;  Score 1280;  DB 6;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
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Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
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Db        320 T 320


RESULT 11
US-10-204-268A-4
; Sequence 4, Application US/10204268A
; Publication No. US20050058647A1
; GENERAL INFORMATION:
;  APPLICANT: KLUXEN, FRANZ-WERNER
;  APPLICANT:  HENTSCH, BERND
;  TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
;  FILE REFERENCE: MERCK-2484
;  CURRENT APPLICATION NUMBER: US/10/204,268A
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: PCT/EP01/01858
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: EP 00103655.7
;  PRIOR FILING DATE: 2000-02-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (188)
;   OTHER INFORMATION: Pro or His
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (387)
;   OTHER INFORMATION: Val, Ala, Asp, Glu or Gly
US-10-204-268A-4

  Query Match            74.4%;  Score 1145;  DB 5;  Length 391;
  Best Local Similarity   99.5%;  Pred. No. 3.2e-112;
  Matches  216;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         52 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 111
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Db         10 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 69

Qy        112 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 129

Qy        172 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHH 231
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        130 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNXH 189

Qy        232 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
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Db        190 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 226
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RESULT 12
US-10-771-833-23
; Sequence 23, Application US/10771833
; Publication No. US20050048573A1
; GENERAL INFORMATION:
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
; FILE REFERENCE: 039363-1106
; CURRENT APPLICATION NUMBER: US/10/771,833
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: 60/444,734
; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-833-23

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  Query Match             63.6%;  Score 980;  DB 5;  Length 335;
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  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 60

Qy        147 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 206
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Db         61 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 120

Qy        207 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 266
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Db        121 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 180

Qy        267 MT 268
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Db        181 MT 182
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RESULT 13
US-10-886-949-23
; Sequence 23, Application US/10886949
; Publication No. US20050079548A1
; GENERAL INFORMATION:
; APPLICANT: DEAN R. ARTIS
; APPLICANT: BOLLAG, GIDEON
; APPLICANT: CARD, GRAHAM
; APPLICANT: MARTIN, FERNANDO
; APPLICANT: MILBURN, MICHAEL V.
; APPLICANT: ZHANG, KAM
; TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
; FILE REFERENCE: 039363-1108
; CURRENT APPLICATION NUMBER: US/10/886,949
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: 60/485,627
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-949-23

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  Query Match             63.6%;  Score 980;  DB 5;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-95;
  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 146
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Db          1 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 60

Qy        147 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 206
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Qy        207 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 266
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Qy        267 MT 268
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Db        181 MT 182
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RESULT 14
US-10-380-437-6
; Sequence 6, Application US/10380437
; Publication No. US20050058998A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A
; APPLICANT: Seebeck, Thomas
; APPLICANT: Soderling, Scott Haydn
; APPLICANT: Rascon, Ana
; APPLICANT: Zoraghi, Roya
; APPLICANT: Kunz, Stefan
; APPLICANT: Gong, Kewei
; APPLICANT: Glavas, Natalie
; TITLE OF INVENTION: NOVEL PDEs AND USES THEREOF
; FILE REFERENCE: 30429.3WO01
; CURRENT APPLICATION NUMBER: US/10/380,437
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/232,445
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/240,500
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-437-6

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  Query Match             58.9%;  Score 907;  DB 5;  Length 424;
  Best Local Similarity   64.6%;  Pred. No. 5.9e-87;
  Matches  168;  Conservative   39;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||       |::||:|| |||: || ||| |:||||||||||
Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKE 266
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Db        286 WRSAVGLLRESGLFSHLPLE 305
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; Sequence 53, Application US/10380437
; Publication No. US20050058998A1
; GENERAL INFORMATION:
;  APPLICANT: Beavo, Joseph A
;  APPLICANT:  Seebeck, Thomas
;  APPLICANT:  Soderling, Scott Haydn
;  APPLICANT:  Rascon, Ana
;  APPLICANT:  Zoraghi, Roya
;  APPLICANT:  Kunz, Stefan
;  APPLICANT:  Gong, Kewei
;  APPLICANT:  Glavas, Natalie
;  TITLE OF INVENTION: NOVEL PDEs AND USES THEREOF
;  FILE REFERENCE: 30429.3WO01
;  CURRENT APPLICATION NUMBER: US/10/380,437
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: 60/232,445
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: 60/240,500
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-380-437-53

  Query Match             58.9%;  Score 907;  DB 5;  Length 424;
  Best Local Similarity   64.6%;  Pred. No. 5.9e-87;
  Matches  168;  Conservative   39;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||      |::||:|| |||: || ||| |:||||||||
Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||||:||.||:| |||||||
Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKE 266
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Db        286 WRSAVGLLRESGLFSHLPLE 305


Search completed: March 10, 2006, 20:22:33
Job time : 88.0244 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 20:19:01 ; Search time 11.3171 Seconds
(without alignments)
708.350 Million cell updates/sec

Title: US-10-781-181-3
Perfect score: 1540
Sequence: 1 MSCLMVERCGEILFENPDQN.....GTWDFDIFLFDRLTNGNSLV 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 1280 | 83.1 | 320 | 7 | US-11-226-701-6 | Sequence 6, Appli |
| 2 | 1280 | 83.1 | 502 | 7 | US-11-226-701-4 | Sequence 4, Appli |
| 3 | 331.5 | 21.5 | 747 | 6 | US-10-492-835-8 | Sequence 8, Appli |
| 4 | 331.5 | 21.5 | 747 | 6 | US-10-492-835-15 | Sequence 15, Appl |
| 5 | 331.5 | 21.5 | 747 | 6 | US-10-492-835-27 | Sequence 27, Appl |
| 6 | 330.5 | 21.5 | 507 | 7 | US-11-091-018-10 | Sequence 10, Appl |
| 7 | 330.5 | 21.5 | 585 | 7 | US-11-091-018-9 | Sequence 9, Appli |
| 8 | 330.5 | 21.5 | 673 | 7 | US-11-091-018-6 | Sequence 6, Appli |
| 9 | 330.5 | 21.5 | 687 | 7 | US-11-091-018-8 | Sequence 8, Appli |
| 10 | 330.5 | 21.5 | 745 | 7 | US-11-091-018-4 | Sequence 4, Appli |
| 11 | 330.5 | 21.5 | 748 | 6 | US-10-492-835-12 | Sequence 12, Appl |
| 12 | 330.5 | 21.5 | 748 | 6 | US-10-492-835-28 | Sequence 28, Appl |
| 13 | 330.5 | 21.5 | 809 | 7 | US-11-091-018-2 | Sequence 2, Appli |
| 14 | 314.5 | 20.4 | 736 | 7 | US-11-169-041-207 | Sequence 207, App |
| 15 | 303.5 | 19.7 | 398 | 7 | US-11-123-893-11 | Sequence 11, Appl |
| 16 | 302.5 | 19.6 | 349 | 7 | US-11-123-893-13 | Sequence 13, Appl |
| 17 | 296.5 | 19.3 | 357 | 7 | US-11-123-893-12 | Sequence 12, Appl |
| 18 | 261 | 16.9 | 769 | 7 | US-11-072-512-2646 | Sequence 2646, Ap |
| 19 | 189 | 12.3 | 786 | 7 | US-11-072-512-2944 | Sequence 2944, Ap |
| 20 | 185 | 12.0 | 941 | 6 | US-10-501-035-343 | Sequence 343, App |
| 21 | 176.5 | 11.5 | 854 | 6 | US-10-511-657-4 | Sequence 4, Appli |
| 22 | 98 | 6.4 | 968 | 6 | US-10-501-035-219 | Sequence 219, App |
| 23 | 84 | 5.5 | 635 | 7 | US-11-096-568A-29628 | Sequence 29628, A |
| 24 | 84 | 5.5 | 710 | 7 | US-11-096-568A-29627 | Sequence 29627, A |
| 25 | 82.5 | 5.4 | 418 | 7 | US-11-109-156-2 | Sequence 2, Appli |
| 26 | 81 | 5.3 | 394 | 7 | US-11-096-568A-5451 | Sequence 5451, Ap |
| 27 | 81 | 5.3 | 852 | 6 | US-10-467-657-5004 | Sequence 5004, Ap |
| 28 | 81 | 5.3 | 6738 | 6 | US-10-922-232B-56 | Sequence 56, Appl |
| 29 | 80.5 | 5.2 | 376 | 7 | US-11-098-686-10379 | Sequence 10379, A |
| 30 | 79 | 5.1 | 643 | 7 | US-11-096-568A-27797 | Sequence 27797, A |
| 31 | 77.5 | 5.0 | 418 | 7 | US-11-099-691-1 | Sequence 1, Appli |
| 32 | 76 | 4.9 | 281 | 6 | US-10-467-657-988 | Sequence 988, App |
| 33 | 75.5 | 4.9 | 259 | 7 | US-11-096-568A-5912 | Sequence 5912, Ap |
| 34 | 75.5 | 4.9 | 344 | 6 | US-10-922-232B-61 | Sequence 61, Appl |
| 35 | 75.5 | 4.9 | 398 | 7 | US-11-087-099-1516 | Sequence 1516, Ap |
| 36 | 75.5 | 4.9 | 398 | 7 | US-11-087-099-4038 | Sequence 4038, Ap |
| 37 | 75.5 | 4.9 | 398 | 7 | US-11-087-099-4756 | Sequence 4756, Ap |
| 38 | 75.5 | 4.9 | 398 | 7 | US-11-087-099-8044 | Sequence 8044, Ap |
| 39 | 75.5 | 4.9 | 398 | 7 | US-11-087-099-9817 | Sequence 9817, Ap |
| 40 | 75.5 | 4.9 | 1007 | 7 | US-11-087-099-735 | Sequence 735, App |
| 41 | 74.5 | 4.8 | 276 | 7 | US-11-096-568A-12387 | Sequence 12387, A |
| 42 | 74.5 | 4.8 | 295 | 7 | US-11-096-568A-12386 | Sequence 12386, A |
| 43 | 74.5 | 4.8 | 380 | 7 | US-11-096-568A-27808 | Sequence 27808, A |
| 44 | 73.5 | 4.8 | 443 | 7 | US-11-087-099-7032 | Sequence 7032, Ap |
| 45 | 73.5 | 4.8 | 443 | 7 | US-11-087-099-7719 | Sequence 7719, Ap |

ALIGNMENTS

RESULT 1
US-11-226-701-6
; Sequence 6, Application US/11226701
; Publication No. US20060009632A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-021OMNIM
; CURRENT APPLICATION NUMBER: US/11/226,701
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: US/10/386,414
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-226-701-6

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  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
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Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
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Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 2
US-11-226-701-4
; Sequence 4, Application US/11226701
; Publication No. US20060009632A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Robison, Keith E.
;  APPLICANT:  White, David
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Cook, William James
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
;  TITLE OF INVENTION:  55092 AND 10218 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-021OMNIM
;  CURRENT APPLICATION NUMBER: US/11/226,701
;  CURRENT FILING DATE:  2005-09-14
;  PRIOR APPLICATION NUMBER: US/10/386,414
;  PRIOR FILING DATE: 2003-03-11
;  PRIOR APPLICATION NUMBER: 09/426,282
;  PRIOR FILING DATE: 1999-10-25
;  PRIOR APPLICATION NUMBER: 09/668,266
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/330,970
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: 09/724,599
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/860,193
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: 09/571,689
;  PRIOR FILING DATE: 2000-05-16
;  PRIOR APPLICATION NUMBER: 10/283,023
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,044
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/010,943
;  PRIOR FILING DATE: 2001-12-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-11-226-701-4

  Query Match             83.1%;  Score 1280;  DB 7;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-123;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320


RESULT 3
US-10-492-835-8
; Sequence 8, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-492-835-8

  Query Match             21.5%;  Score 331.5;  DB 6;  Length 747;
  Best Local Similarity   37.8%;  Pred. No. 8.7e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |  :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :|||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        469 VLENHHLAVGFKLLQE 484


RESULT 4
US-10-492-835-15
; Sequence 15, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
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;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Murine sp.
US-10-492-835-15

  Query Match             21.5%;  Score 331.5;  DB 6;  Length 747;
  Best Local Similarity   37.8%;  Pred. No. 8.7e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
                |:| || :|     ::  |:| |    ||: :    || | :    | | |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRE 256
                ||||||      :|:|
Db        469 VLENHHLAVGFKLLQE 484


RESULT 5
US-10-492-835-27
; Sequence 27, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-492-835-27

  Query Match             21.5%;  Score 331.5;  DB 6;  Length 747;
  Best Local Similarity   37.8%;  Pred. No. 8.7e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
                |:| || :|     ::  |:| |    ||:  :    || | :    | | |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||:: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRE 256
                ||||||      :|:|
Db        469 VLENHHLAVGFKLLQE 484


RESULT 6
US-11-091-018-10
; Sequence 10, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-10

  Query Match             21.5%;  Score 330.5;  DB 7;  Length 507;
  Best Local Similarity   37.8%;  Pred. No. 6.6e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
                |:| || :|     ::  |:| |    ||:  :    || | :    | | |   :|
Db         52 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 108

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        109 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 167

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        168 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 227

Qy        241 VLENHHWRSTIGMLRE 256
                ||||||      :|:|
Db        228 VLENHHLAVGFKLLQE 243


RESULT 7
US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
```

```
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 585
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-9

  Query Match            21.5%;  Score 330.5;  DB 7;  Length 585;
  Best Local Similarity  37.8%;  Pred. No. 8e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        130 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 186

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        187 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 245

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        246 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 305

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        306 VLENHHLAVGFKLLQE 321


RESULT 8
US-11-091-018-6
; Sequence 6, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 673
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-6

  Query Match            21.5%;  Score 330.5;  DB 7;  Length 673;
  Best Local Similarity  37.8%;  Pred. No. 9.6e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        394 VLENHHLAVGFKLLQE 409


RESULT 9
US-11-091-018-8
; Sequence 8, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 687
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-8

  Query Match            21.5%;  Score 330.5;  DB 7;  Length 687;
  Best Local Similarity  37.8%;  Pred. No. 9.9e-26;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        232 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 288

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        289 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 347

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        348 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 407

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        408 VLENHHLAVGFKLLQE 423


RESULT 10
US-11-091-018-4
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; Sequence 4, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 745
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-4

  Query Match             21.5%;  Score 330.5;  DB 7;  Length 745;
  Best Local Similarity   37.8%;  Pred. No. 1.1e-25;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        290 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 346

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        347 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 405

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        406 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 465

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        466 VLENHHLAVGFKLLQE 481


RESULT 11
US-10-492-835-12
; Sequence 12, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 748
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-492-835-12

  Query Match             21.5%;  Score 330.5;  DB 6;  Length 748;
  Best Local Similarity   37.8%;  Pred. No. 1.1e-25;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        469 VLENHHLAVGFKLLQE 484


RESULT 12
US-10-492-835-28
; Sequence 28, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
;   LENGTH: 748
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-492-835-28

  Query Match             21.5%;  Score 330.5;  DB 6;  Length 748;
  Best Local Similarity   37.8%;  Pred. No. 1.1e-25;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||      :|:|
Db        469 VLENHHLAVGFKLLQE 484


RESULT 13
US-11-091-018-2
; Sequence 2, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
```

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;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 809
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-2

  Query Match             21.5%;  Score 330.5;  DB 7;  Length 809;
  Best Local Similarity   37.8%;  Pred. No. 1.2e-25;
  Matches   74;  Conservative   35;  Mismatches   78;  Indels    9;  Gaps    4;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :   | |  |   :|
Db        354 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 410

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        411 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 469

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| |||||||:  ||| ||  || :| : |
Db        470 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 529

Qy        241 VLENHHWRSTIGMLRE 256
              ||||||     :|:|
Db        530 VLENHHLAVGFKLLQE 545


RESULT 14
US-11-169-041-207
; Sequence 207, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;  TITLE OF INVENTION:  COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;  TITLE OF INVENTION:  KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 10001 NP
;  CURRENT APPLICATION NUMBER: US/11/169,041
;  CURRENT FILING DATE:  2005-06-28
;  PRIOR APPLICATION NUMBER: 60/584,405
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 527
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-169-041-207

  Query Match             20.4%;  Score 314.5;  DB 7;  Length 736;
  Best Local Similarity   33.6%;  Pred. No. 4.8e-24;
  Matches   71;  Conservative   44;  Mismatches   87;  Indels    9;  Gaps    3;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::     ::  |:| |    | :  ::  :||:| :    |:|   |  :||
Db        298 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 354

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                 ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||
Db        355 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 414

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
              |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        415 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 474

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTGT 270
              |||||      :|:|    :  :| |:   |
Db        475 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQT 505


RESULT 15
US-11-123-893-11
; Sequence 11, Application US/11123893
; Publication No. US20060041006A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA
;  APPLICANT:  CHO, HANNA
;  APPLICANT:  ENGLAND, BRUCE
;  APPLICANT:  GILLETTE, SAM
;  APPLICANT:  ARTIS, DEAN RICHARD
;  APPLICANT:  ZUCKERMAN, REBECCA
;  APPLICANT:  ZHANG, CHAO
;  TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
;  FILE REFERENCE: 039363-1109
;  CURRENT APPLICATION NUMBER: US/11/123,893
;  CURRENT FILING DATE:  2005-05-06
;  PRIOR APPLICATION NUMBER: 60/569,435
;  PRIOR FILING DATE: 2004-05-06
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-123-893-11

  Query Match             19.7%;  Score 303.5;  DB 7;  Length 398;
  Best Local Similarity   32.9%;  Pred. No. 2.8e-23;
  Matches   68;  Conservative   41;  Mismatches   81;  Indels   17;  Gaps    4;

Qy         74 SFQRYFHASRLLRGIIPQAP--------LHLLDEDYLGQARHMLSKVGMWDFDIFLFDRL 125
              |   : |:|    |::|:           ::  :||:| :    |:|   | :||
Db          4 SHHHHHHSS----GLVPRGSHMSISRFGVNTENEDHLAKELEDLNK---WGLNIFNVAGY 56

Qy        126 TNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAM 185
              ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||  |:
Db         57 SHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQST 116

Qy        186 HCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENH 245
              |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||||||
Db        117 HVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENH 176

Qy        246 HWRSTIGMLRESR--LLAHLPKEMTGT 270
              |      :|:|    :  :| |:   |
Db        177 HLAVGFKLLQEEHCDIFMNLTKKQRQT 203


Search completed: March 10, 2006, 20:23:09
Job time : 13.3171 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:00 ; Search time 166.463 Seconds
(without alignments)
1187.771 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2408 | 100.0 | 450 | 3 | AAY93569 | Aay93569 Amino aci |
| 2 | 2408 | 100.0 | 450 | 4 | AAU08675 | Aau08675 Human pho |
| 3 | 2408 | 100.0 | 450 | 4 | AAG78915 | Aag78915 Human typ |
| 4 | 2401 | 99.7 | 450 | 8 | ADP79549 | Adp79549 Human pho |
| 5 | 2258 | 93.8 | 502 | 5 | ABB09005 | Abb09005 Human pho |
| 6 | 2258 | 93.8 | 502 | 8 | ADJ58904 | Adj58904 Human cyc |
| 7 | 2234 | 92.8 | 502 | 4 | AAB36503 | Aab36503 Human lon |
| 8 | 2219.5 | 92.2 | 451 | 3 | AAY93575 | Aay93575 Amino aci |
| 9 | 2192 | 91.0 | 446 | 3 | AAY93567 | Aay93567 Amino aci |
| 10 | 2166 | 90.0 | 446 | 3 | AAY93574 | Aay93574 Amino aci |
| 11 | 2165.5 | 89.9 | 445 | 3 | AAY93573 | Aay93573 Amino aci |
| 12 | 2121 | 88.1 | 437 | 3 | AAY93572 | Aay93572 Amino aci |
| 13 | 1990.5 | 82.7 | 413 | 3 | AAY93571 | Aay93571 Amino aci |
| 14 | 1865 | 77.5 | 391 | 4 | AAU08676 | Aau08676 Human pho |
| 15 | 1801 | 74.8 | 335 | 9 | ADY50214 | Ady50214 Human PDE |
| 16 | 1801 | 74.8 | 335 | 9 | ADZ46770 | Adz46770 Human PDE |
| 17 | 1430 | 59.4 | 268 | 3 | AAY93593 | Aay93593 Amino aci |
| 18 | 1430 | 59.4 | 288 | 3 | AAY93568 | Aay93568 Amino aci |
| 19 | 1425.5 | 59.2 | 456 | 5 | AAE24530 | Aae24530 Mouse PDE |
| 20 | 1419.5 | 58.9 | 482 | 5 | AAE24531 | Aae24531 Human PDE |
| 21 | 1419.5 | 58.9 | 482 | 8 | ADO40842 | Ado40842 Human pho |
| 22 | 1419.5 | 58.9 | 482 | 8 | ADR46207 | Adr46207 Human pho |
| 23 | 1419.5 | 58.9 | 482 | 9 | ADY18092 | Ady18092 PRO polyp |
| 24 | 1419.5 | 58.9 | 498 | 2 | AAW00094 | Aaw00094 cAMP phos |
| 25 | 1419.5 | 58.9 | 498 | 2 | AAY49808 | Aay49808 Human gli |
| 26 | 1419.5 | 58.9 | 498 | 3 | AAB20619 | Aab20619 pTM22 hum |
| 27 | 1419.5 | 58.9 | 498 | 8 | ADR66097 | Adr66097 Human pro |
| 28 | 1419.5 | 58.9 | 498 | 8 | ADR66439 | Adr66439 Human pro |
| 29 | 1418.5 | 58.9 | 456 | 8 | ADO21910 | Ado21910 Human cAM |
| 30 | 1418.5 | 58.9 | 456 | 9 | ADY18172 | Ady18172 PRO polyp |
| 31 | 1410.5 | 58.6 | 426 | 5 | AAE24528 | Aae24528 Mouse PDE |
| 32 | 1403.5 | 58.3 | 426 | 5 | AAE24527 | Aae24527 Human PDE |
| 33 | 1403.5 | 58.3 | 446 | 5 | AAE24532 | Aae24532 Human PDE |
| 34 | 1402.5 | 58.2 | 468 | 8 | ABM83120 | Abm83120 Human dia |
| 35 | 1397.5 | 58.0 | 426 | 5 | AAE24529 | Aae24529 Rat PDE7 |
| 36 | 1397.5 | 58.0 | 428 | 5 | AAE24533 | Aae24533 Rat PDE7a |
| 37 | 1297 | 53.9 | 441 | 8 | ABM83121 | Abm83121 Human dia |
| 38 | 1287 | 53.4 | 424 | 5 | AAU79727 | Aau79727 Human cyc |
| 39 | 1286 | 53.4 | 432 | 4 | AAU16967 | Aau16967 Human nov |
| 40 | 1280 | 53.2 | 320 | 4 | AAB36504 | Aab36504 Human sho |
| 41 | 1280 | 53.2 | 320 | 8 | ADJ58906 | Adj58906 Human cyc |
| 42 | 1277 | 53.0 | 425 | 8 | ABM83119 | Abm83119 Human dia |
| 43 | 1261 | 52.4 | 437 | 8 | ABM83118 | Abm83118 Human dia |
| 44 | 1240.5 | 51.5 | 359 | 8 | ADR46209 | Adr46209 Human pho |
| 45 | 1239.5 | 51.5 | 354 | 8 | ADR46211 | Adr46211 Human pho |

ALIGNMENTS

RESULT 1
AAY93569
ID AAY93569 standard; protein; 450 AA.
XX
AC AAY93569;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human phosphodiesterase enzyme.
XX
KW Phosphodiesterase; PDE-XIV; human; enzyme.
XX
OS Homo sapiens.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PF 09-NOV-1999; 99EP-00308902.
XX
PR 23-DEC-1998; 98GB-00028603.
PR 17-SEP-1999; 99GB-00022123.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Fidock M;
XX
DR WPI; 2000-433274/38.
DR N-PSDB; AAA46651.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity.
XX
PS Disclosure; Page 45-47; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide be
CC administered to treat diseases by rectifying mutations or deletions in a
CC patient's genome that affect the activity of PDE-XIV. They may also be
CC used to study the expression and function of PDE-XIV polypeptides and
CC their role in metabolism. The PDE-XIV polypeptides may be used as
CC antigens in the production of antibodies against PDE-XIV and in assays to
CC identify modulators (agonists and antagonists) of PDE-XIV expression and

```
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 450 AA;

  Query Match            100.0%;  Score 2408;  DB 3;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-226;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 2
AAU08675
ID   AAU08675 standard; protein; 450 AA.
XX
AC   AAU08675;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human phosphodiesterase type 7B #1.
XX
KW   Human; phosphodiesterase type 7B; cardiovascular disease; asthma;
KW   allergy; inflammatory disease; immune-related disorder; cardiovascular;
KW   antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO200162940-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-EP001858.
XX
PR   21-FEB-2000; 2000EP-00103655.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Kluxen F,  Hentsch B;
XX
DR   WPI; 2001-570636/64.
DR   N-PSDB; AAS13248.
XX
PT   Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
PT   diagnosing and treating, e.g. asthma, inflammation and allergies.
XX
PS   Claim 1; Page 36-37; 40pp; English.
XX
CC   The invention relates to a novel human Phosphodiesterase type 7B
CC   polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC   acid may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC   example, The protein and nucleic acid may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P7B by expressing
CC   inactive proteins or to supplement the patients own production of P7B.
CC   The nucleic acids may be used to produce P7B polypeptides, by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. The nucleic acid and its complements may also be used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acids in samples, and therefore which patients may be in
CC   need of restorative therapy. The P7B polypeptides may also be used as
CC   antigens in the production of antibodies against P7B and in assays to
CC   identify modulators of it's expression and activity. The anti-P7B
CC   antibodies and antagonists may also be used to down regulate expression
CC   and activity. The anti-P7B antibodies may also be used as diagnostic
CC   agents for detecting the presence of P7B in samples (e.g. by enzyme
CC   linked immunosorbent assay (ELISA)). Disorders that may be prevented,
CC   diagnosed and/or treated by the above methods include, for example
CC   cardiovascular disease, asthma, allergy, inflammation, and immune-related
CC   disorders. The present sequence represents a human phosphodiesterase 7B
XX
SQ   Sequence 450 AA;

  Query Match            100.0%;  Score 2408;  DB 4;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-226;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
```

```
RESULT 3
AAG78915
ID   AAG78915 standard; protein; 450 AA.
XX
AC   AAG78915;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Human type 7B phosphodiesterase, PDE7B.
XX
KW   Human; type 7B phosphodiesterase; PDE7B; enzyme.
XX
OS   Homo sapiens.
XX
PN   JP2001238680-A.
XX
PD   04-SEP-2001.
XX
PF   03-MAR-2000; 2000JP-00058159.
XX
PR   03-MAR-2000; 2000JP-00058159.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
DR   WPI; 2001-610057/70.
DR   N-PSDB; AAI70009.
XX
PT   New phosphodiesterase for use in the development of inhibitors of high
PT   selectivity and drugs of low side effect.
XX
PS   Claim 2; Page 12-14; 18pp; Japanese.
XX
CC   The present sequence is the protein sequence for human type 7B
CC   phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the
CC   development of inhibitors of high selectivity and drugs of low side
CC   effects
XX
SQ   Sequence 450 AA;

  Query Match           100.0%;  Score 2408;  DB 4;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-226;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 4
ADP79549
ID   ADP79549 standard; protein; 450 AA.
XX
AC   ADP79549;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human phosphodiesterase 7B nucleotide sequence.
XX
KW   Human; phosphodiesterase 7B; PDE7b; cardiovascular-gen.; CNS-Gen.;
KW   gynaecological; haemostatic; respiratory-Gen.; cytostatic; gene therapy;
KW   enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2004044196-A1.
XX
PD   27-MAY-2004.
XX
PF   05-NOV-2003; 2003WO-EP012342.
XX
PR   13-NOV-2002; 2002EP-00025502.
XX
PA   (FARB ) BAYER HEALTHCARE AG.
XX
PI   Golz S,  Brueggemeier U,  Summer H;
XX
DR   WPI; 2004-440631/41.
DR   N-PSDB; ADP79548.
XX
PT   Screening for therapeutic agents, useful in treating cardiovascular,
PT   reproduction, urological, hematological, respiratory system or cancer
PT   diseases, comprises contacting a test compound with a phosphodiesterase
PT   7b.
XX
PS   Disclosure; SEQ ID NO 2; 128pp; English.
XX
CC   The present sequence is that of human phosphodiesterase 7b (PDE7b), an
CC   enzyme regulating intracellular levels of cAMP and cGMP. The invention
CC   relates to novel disease associations of PDE7b polynucleotides and
CC   polypeptides. It also relates to novel methods of screening for
CC   therapeutic agents for the treatment of cardiovascular diseases,
CC   disorders of the peripheral and central nervous system, reproduction
CC   diseases, urological diseases, haematological diseases, disorders of the
CC   respiratory system and cancer. PDE7b polynucleotides, polypeptides and
CC   regulators or modulators of PDE7b activity (e.g. an RNA molecule,
CC   antisense oligonucleotide, polypeptide, antibody or ribozyme) can be used
CC   in the treatment or diagnosis of these diseases and disorders.
XX
SQ   Sequence 450 AA;

  Query Match           99.7%;  Score 2401;  DB 8;  Length 450;
  Best Local Similarity  99.8%;  Pred. No. 7.6e-226;
  Matches  449;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
```

```
Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFYGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
```

RESULT 5
ABB09005
ID  ABB09005 standard; protein; 502 AA.
XX
AC  ABB09005;
XX
DT  23-MAY-2002  (first entry)
XX
DE  Human phosphodiesterase-1.
XX
KW  HPDE; human phosphodiesterase; cyclic nucleotide phosphodiesterase;
KW  antiinflammatory; neuroprotective; cytostatic; antianaemic;
KW  immunosuppressive; HIV; cardiovascular disorder; mental disorder;
KW  gene therapy; transgene; enzyme.
XX
OS  Homo sapiens.
XX
PN  WO200198471-A2.
XX
PD  27-DEC-2001.
XX
PF  21-JUN-2001; 2001WO-US020140.
XX
PR  22-JUN-2000; 2000US-0213741P.
PR  14-JUL-2000; 2000US-0218234P.
PR  16-OCT-2000; 2000US-0241100P.
XX
PA  (INCY-) INCYTE GENOMICS INC.
XX
PI  Thornton M, Ding L, Patterson C, Yao MG, Tribouley CM, Lal P;
PI  Hafalia AJA, Baughn MR, Ramkumar J, Lu Y, Walia NK;
XX
DR  WPI; 2002-147799/19.
DR  N-PSDB; ABA99136.
XX
PT  Novel human phosphodiesterase polypeptides and polynucleotides for
PT  diagnosing, preventing and treating eye, neurological, cardiovascular,
PT  cell proliferative and autoimmune/inflammatory disorders.
XX
PS  Claim 1; Page 97-98; 105pp; English.
XX
CC  This invention relates to isolated human phosphodiesterase polypeptides
CC  (HPDE 1-4), which are antiinflammatory, neuroprotective, cytostatic,
CC  antianaemic, immunosuppressive and anti-HIV in their action. The
CC  polypeptides are useful for screening a compound for effectiveness as an
CC  agonist or antagonist of the protein. The identified agonist, antagonist
CC  and protein are useful for treating a disease or condition associated
CC  with decreased or overexpression of functional HPDE in a patient. The
CC  proteins are useful in preparing polyclonal or monoclonal antibodies by
CC  hybridoma technology. They are also useful in the treatment and
CC  prevention of eye, neurological, cardiovascular, cell proliferative and
CC  autoimmune and inflammatory disorders, metabolic disorders and mental
CC  disorders. The polynucleotides are useful for creating humanised animals
CC  or transgenic animals to model human disease and to detect and quantify
CC  gene expression in biopsied tissues in which expression of HPDE is
CC  correlated with disease. HPDE, its fragments and antibodies specific for
CC  HPDE are useful as elements on a microarray which is useful to monitor or
CC  measure protein-protein interactions, drug-target interactions and gene
CC  expression profiles. This sequence represents HPDE-1
XX
SQ  Sequence 502 AA;

```
  Query Match             93.8%;  Score 2258;  DB 5;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 9e-212;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
              |||
Db        500 DSP 502
```

RESULT 6
ADJ58904
ID  ADJ58904 standard; protein; 502 AA.
XX
AC  ADJ58904;
XX
DT  06-MAY-2004  (first entry)
XX
DE  Human cyclic nucleotide phosphodiesterase protein #1.
XX
KW  27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;
KW  cellular proliferation; cellular differentiation; immune disorder;
KW  cardiovascular disorder; endothelial cell disorder;
KW  haematopoietic disorder; blood vessel disorder; brain disorder; pain;
KW  metabolic disorder; liver disorder; platelet disorder; gene therapy;
KW  human; cyclic; enzyme.
XX
OS  Homo sapiens.
XX
PN  US2004006016-A1.
XX
PD  08-JAN-2004.
XX
PF  11-MAR-2003; 2003US-00386414.
XX
PR  11-JUN-1999;  99US-00330970.

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PR   25-OCT-1999;   99US-00426282.
PR   16-MAY-2000; 2000US-00571689.
PR   22-SEP-2000; 2000US-00668266.
PR   28-NOV-2000; 2000US-00724599.
PR   07-DEC-2000; 2000US-0254037P.
PR   10-APR-2001; 2001US-00833082.
PR   16-MAY-2001; 2001US-00860193.
PR   31-OCT-2001; 2001US-0335044P.
PR   06-DEC-2001; 2001US-00010943.
PR   29-OCT-2002; 2002US-00283023.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D,  Robison KE,  Macbeth KJ,  Carroll JM;
PI   Cook WJ,  Meyers RE,  Chun M,  Williamson MJ;
XX
DR   WPI; 2004-081738/08.
DR   N-PSDB; ADJ58903.
XX
PT   New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic
PT   acid molecules, useful for diagnosing or treating cancer, pain, or
PT   immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
PT   and liver disorders.
XX
PS   Claim 4; SEQ ID NO 4; 245pp; English.
XX
CC   The present invention relates to an isolated 27875, 22025, 27420, 17906,
CC   16319, 55092, or 10218 nucleic acid molecule. The invention is useful for
CC   diagnosing or treating cancer or aberrant cellular proliferation and/or
CC   differentiation, immune disorders, heart disorders, cardiovascular
CC   disorders including endothelial cell disorders, haematopoietic disorders,
CC   blood vessel disorders, brain disorders, pain and metabolic disorders,
CC   liver disorders and platelet disorders. The invention is also useful in
CC   gene therapy. The present sequence is human cyclic nucleotide
CC   phosphodiesterase.
XX
SQ   Sequence 502 AA;

  Query Match             93.8%;  Score 2258;  DB 8;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 9e-212;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
              |||
Db        500 DSP 502
```

```
RESULT 7
AAB36503
ID   AAB36503 standard; protein; 502 AA.
XX
AC   AAB36503;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Human long phosphodiesterase protein SEQ ID NO:1.
XX
KW   Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
KW   cyclic nucleotide phosphodiesterase; nootropic; cardiant; hypotensive;
KW   nephrotropic; antidepressant; antiinflammatory; immunosuppressive;
KW   antiinfertility; antiasthmatic; vasotropic; gene therapy; dementia;
KW   amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
KW   glomerulonephritis; bipolar depression; bronchial asthma; salt retention;
KW   atopic disease; autoimmune encephalomyelitis; organ transplantation;
KW   nephrotic syndrome; erectile dysfunction.
XX
OS   Homo sapiens.
XX
PN   US6146876-A.
XX
PD   14-NOV-2000.
XX
PF   11-JUN-1999;   99US-00330970.
XX
PR   26-MAR-1999;   99US-00277423.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  White D,  Robision KE;
XX
DR   WPI; 2001-023577/03.
DR   N-PSDB; AAC87948.
XX
PT   Polynucleotide encoding novel cyclic nucleotide phosphodiesterase useful
PT   for treating disorders related with to protein e.g. dementia,
PT   hypertension, glomerulonephritis, and organ transplantation.
XX
PS   Claim 3; Fig 1; 42pp; English.
XX
CC   The present sequence represents the human long phosphodiesterase which is
CC   a cyclic nucleotide phosphodiesterase (I). (I) can have nootropic,
CC   cardiant, hypotensive, nephrotropic, antidepressant, antiinflammatory,
CC   immunosuppressive, antiinfertility, antiasthmatic and vasotropic
CC   activities, and can be used in gene therapy. (I) can be used for treating
CC   various disorders associated or mediated by (I), such as dementia,
CC   amnesia, congestive heart failure, thrombosis, pulmonary hypertension,
CC   glomerulonephritis, bipolar depression, bronchial asthma, atopic
CC   diseases, autoimmune encephalomyelitis, organ transplantation, salt
CC   retention in nephrotic syndrome and erectile dysfunction
XX
SQ   Sequence 502 AA;

  Query Match             92.8%;  Score 2234;  DB 4;  Length 502;
  Best Local Similarity   99.1%;  Pred. No. 2e-209;
  Matches  419;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQIGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259
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Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLGALYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIAWKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
              |||
Db        500 DSP 502
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RESULT 8
AAY93575
ID   AAY93575 standard; protein; 451 AA.
XX
AC   AAY93575;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 21
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 169
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 307
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 308
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 419
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 435
FT                   /label= His, Leu
FT   Misc-difference 438. .440
FT                   /note= "these residues are either Gln-Gly-Pro or Pro-Ala-
FT                   Pro"
FT   Misc-difference 442. .443
FT                   /note= "these residues are either Ser-Glu or Thr-Leu"
FT   Misc-difference 446
FT                   /note= "optionally absent"
FT   Misc-difference 449. .450
FT                   /note= "these residues are either Asp-Ser or Ala-Thr"
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 75-78; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 451 AA;
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```
  Query Match            92.2%;  Score 2219.5;  DB 3;  Length 451;
  Best Local Similarity  93.1%;  Pred. No. 4.6e-208;
  Matches  420;  Conservative    0;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| ||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
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```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                |||||||||||||||||| |||||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
                ||||||  |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 KDLRLEXXQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGXLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
                |||||||||||||||||| |||||||||| |||||||||||| ||||||||||||   |
Db        361 PLCNQQKDSIPSIQIGFMXYIVEPLFREWAXFTGNSTLSENMLXHLAHNKAQWKSLLXXQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
                || |||||||||| ||   |  || ||  |
Db        421 HRXRGSSGSGPDHDXAGXXXEXXEQTEGXXP 451


RESULT 9
AAY93567
ID   AAY93567 standard; protein; 446 AA.
XX
AC   AAY93567;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a murine phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; murine; enzyme.
XX
OS   Mus sp.
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
DR   N-PSDB; AAA46649.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 39-41; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 446 AA;

  Query Match             91.0%;  Score 2192;  DB 3;  Length 446;
  Best Local Similarity   91.6%;  Pred. No. 2.2e-205;
  Matches  413;  Conservative   13;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||:|||:|:|: ||||||||:|||||||| ||||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||:|||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||: |||||||||||||||||||||||||||||||||||||||||:||||||||||
Db        301 KDLRLENVQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              |||||||||||||||:|||||||||| |||||||||||| |||||||||||||   |
Db        361 PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
              || |||       | ||   |: || || :|
Db        421 HRRRGSG-----QDLAGPAPETLEQTEGATP 446


RESULT 10
AAY93574
ID   AAY93574 standard; protein; 446 AA.
XX
AC   AAY93574;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20
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FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 21
FT                   /label= Ser, Val, Asn, Ala
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 169
FT                   /label= Gly, His, Ser, Gln
FT   Misc-difference 307
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 308
FT                   /label= Asp, Ala, Asn, Val
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 419
FT                   /label= Pro, Arg, Ser, Asn
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 430
FT                   /label= His, Leu
FT   Misc-difference 433
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT   Misc-difference 434
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT   Misc-difference 435
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT   Misc-difference 437
FT                   /label= Ser, Glu, Thr, Leu
FT   Misc-difference 438
FT                   /label= Ser, Glu, Thr, Leu
FT   Misc-difference 441
FT                   /note= "optionally absent"
FT   Misc-difference 444
FT                   /label= Asp, Ser, Ala, Thr
FT   Misc-difference 445
FT                   /label= Asp, Ser, Ala, Thr
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 70-72; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 446 AA;

  Query Match             90.0%;  Score 2166;  DB 3;  Length 446;
  Best Local Similarity   91.6%;  Pred. No. 7.8e-203;
  Matches  413;  Conservative    0;  Mismatches   32;  Indels    6;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||  ||| | |  |||||||| |||||||| |||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||  |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 KDLRLEXXQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGXLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              |||||||||||||||| |||||||||| |||||||||| ||||||||||||  |
Db        361 PLCNQQKDSIPSIQIGFMXYIVEPLFREWAXFTGNSTLSENMLXHLAHNKAQWKSLLXXQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
              || |||       | ||    |  || ||  |
Db        421 HRXRGSG-----QDXAGXXXEXXEQTEGXXP 446


RESULT 11
AAY93573
ID   AAY93573 standard; protein; 445 AA.
XX
AC   AAY93573;
XX
DT   25-SEP-2000  (first entry)
XX
```

```
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /label= Val, Ile
FT   Misc-difference 16
FT                   /label= Ser, Asn
FT   Misc-difference 18
FT                   /label= Glu, Asp
FT   Misc-difference 20. .21
FT                   /label= Ser, Val, Asn, Ala
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 30
FT                   /label= Val, Ile
FT   Misc-difference 39
FT                   /label= Pro, Arg
FT   Misc-difference 56
FT                   /label= Asn, Ser
FT   Misc-difference 59
FT                   /label= His, Tyr
FT   Misc-difference 114
FT                   /label= Thr, Met
FT   Misc-difference 141
FT                   /label= Ser, Thr
FT   Misc-difference 168. .169
FT                   /label= Gly, His, Ser, Gln
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 307. .308
FT                   /label= Asp, Ala, Asn, Val
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 350
FT                   /label= Glu, Asp
FT   Misc-difference 379
FT                   /label= Ser, Thr
FT   Misc-difference 391
FT                   /label= His, Arg
FT   Misc-difference 404
FT                   /label= Gly, Ser
FT   Misc-difference 418. .419
FT                   /label= Pro, Arg, Ser, Asn
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 423
FT                   /label= Ser, Arg
FT   Misc-difference 423
FT   Misc-difference 427. .428
FT                   /label= Ser, Gly, Pro, Asp, His, Gln
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 430
FT                   /label= His, Leu
FT   Misc-difference 433. .434
FT                   /label= Gln, Gly, Thr, Pro, Ala
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 436. .437
FT                   /label= Ser, Glu, Thr, Leu
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
FT   Misc-difference 440
FT                   /note= "optiqnally absent"
FT   Misc-difference 443. .444
FT                   /label= Asp, Ser, Ala, Thr
FT                   /note= "these residues are a peptide comprising at least
FT                   two or more of the above residues"
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 64-66; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 445 AA;

  Query Match            89.9%;  Score 2165.5;  DB 3;  Length 445;
  Best Local Similarity  91.3%;  Pred. No. 8.7e-203;
  Matches  411;  Conservative    1;  Mismatches   33;  Indels    5;  Gaps    1;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| |||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQXXKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHXXNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||  |||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 KDLRLEXXQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGXLEQKFELEIS 360
```

```
Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||| |||||||||| |||||||||||| ||||||||||||   |
Db        361 PLCNQQKDSIPSIQIGFMXYIVEPLFREWAXFTGNSTLSENMLXHLAHNKAQWKSLLXXQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              || |||       | ||     |: ||  |
Db        421 HRXRGSX-----XDXAGXXEXXEQTEGXXP 445


RESULT 12
AAY93572
ID   AAY93572 standard; protein; 437 AA.
XX
AC   AAY93572;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 16
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 18
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 20
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 29
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 38
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 55
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 58
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 113
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 140
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 167
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 305
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 347
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 376
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 388
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 401
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 415
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 419
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 423
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 425
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 428
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 430
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 433
FT                   /note= "any suitable peptide sequence or amino acid"
FT   Misc-difference 436
FT                   /note= "any suitable peptide sequence or amino acid"
XX
```

```
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 58-60; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 437 AA;

  Query Match            88.1%;  Score 2121;  DB 3;  Length 437;
  Best Local Similarity  91.9%;  Pred. No. 1.9e-198;
  Matches  411;  Conservative    1;  Mismatches   23;  Indels   12;  Gaps    6;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| | |  |||||||| |||||||| |||||||||||||||| || |
Db          1 MSCLMVERCGEXLFEXPXQ-XKCVCMLGDXRLRGQTGVXAERRGSYPFIDFRLLNXTTXS 59

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         60 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGXWDFDIF 119

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||||  ||||||||||
Db        120 LFDRLTNGNSLVTLLCHLFNXHGLIHHFKLDMVTLHRFLVMVQEDYHX-NPYHNAVHAAD 178

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 238

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 298

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||  |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        299 KDLRLE-XQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGXLEQKFELEIS 357
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Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||| |||||||||| |||||||||| |||||||||||||   |
Db        358 PLCNQQKDSIPSIQIGFMXYIVEPLFREWAXFTGNSTLSENMLXHLAHNKAQWKSLL-XQ 416

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEG 447
              || |||       | |  | | |: ||
Db        417 HRXRGSX------DXA--GXEXEQXEG 435


RESULT 13
AAY93571
ID   AAY93571 standard; protein; 413 AA.
XX
AC   AAY93571;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; enzyme.
XX
OS   Synthetic.
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Claim 2; Page 55-57; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   enzyme sequence is derived from a formula of the invention. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 413 AA;

  Query Match             82.7%;  Score 1990.5;  DB 3;  Length 413;
  Best Local Similarity   90.8%;  Pred. No. 1.1e-185;
  Matches  406;  Conservative    1;  Mismatches    5;  Indels   35;  Gaps   16;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||| ||| |||||||| |||||||| |||||||||||||||:|  |
Db          1 MSCLMVERCGE-LFE----PQKCVCMLGD-RLRGQTGV-AERRGSYPFIDFRLLNTT--S 51

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         52 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVG-WDFDIF 110

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||| |||||||||||||||||||||  ||||||||||
Db        111 LFDRLTNGNSLVTLLCHLFN-HGLIHHFKLDMVTLHRFLVMVQEDYH--NPYHNAVHAAD 167

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 227

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 287

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||  ||||||||||||||||||||||||||||||||||||||| |||||||||
Db        288 KDLRLE--QDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQG-LEQKFELEIS 344

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              |||||||||||||||||| |||||||||| |||||||||| |||||||||||||   |
Db        345 PLCNQQKDSIPSIQIGFM-YIVEPLFREWA-FTGNSTLSENML-HLAHNKAQWKSLL--Q 399

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEG 447
              || |||                |||||
Db        400 HR-RGSDA-------------GEEQEG 412


RESULT 14
AAU08676
ID   AAU08676 standard; protein; 391 AA.
XX
AC   AAU08676;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human phosphodiesterase type 7B #2.
XX
KW   Human; phosphodiesterase type 7B; cardiovascular disease; asthma;
KW   allergy; inflammatory disease; immune-related disorder; cardiovascular;
KW   antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 188
FT                   /label= Unknown
FT                   /note= "Encoded by CMC"
FT   Misc-difference 188
FT                   /note= "Encoded by GAR"
FT   Misc-difference 387
FT                   /label= Unknown
FT                   /note= "Encoded by GNN"
XX
PN   WO200162940-A2.
XX
PD   30-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-EP001858.
XX
PR   21-FEB-2000; 2000EP-00103655.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Kluxen F, Hentsch B;
XX
DR   WPI; 2001-570636/64.
DR   N-PSDB; AAS13249.
XX
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```
PT   Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
PT   diagnosing and treating, e.g. asthma, inflammation and allergies.
XX
PS   Claim 1; Page 39-40; 40pp; English.
XX
CC   The invention relates to a novel human Phosphodiesterase type 7B
CC   polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC   acid may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC   example, The protein and nucleic acid may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P7B by expressing
CC   inactive proteins or to supplement the patients own production of P7B.
CC   The nucleic acids may be used to produce P7B polypeptides, by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. The nucleic acid and its complements may also be used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acids in samples, and therefore which patients may be in
CC   need of restorative therapy. The P7B polypeptides may also be used as
CC   antigens in the production of antibodies against P7B and in assays to
CC   identify modulators of it's expression and activity. The anti-P7B
CC   antibodies and antagonists may also be used to down regulate expression
CC   and activity. The anti-P7B antibodies may also be used as diagnostic
CC   agents for detecting the presence of P7B in samples (e.g. by enzyme
CC   linked immunosorbent assay (ELISA)). Disorders that may be prevented,
CC   diagnosed and/or treated by the above methods include, for example
CC   cardiovascular disease, asthma, allergy, inflammation, and immune-related
CC   disorders. The present sequence represents a human phosphodiesterase 7B
XX
SQ   Sequence 391 AA;

  Query Match           77.5%;  Score 1865;  DB 4;  Length 391;
  Best Local Similarity   92.7%;  Pred. No. 2e-173;
  Matches  354;  Conservative    2;  Mismatches   26;  Indels    0;  Gaps    0;

Qy         52 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 69

Qy        112 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 129

Qy        172 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHH 231
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        130 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNXH 189

Qy        232 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 249

Qy        292 TRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGEL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGEL 309

Qy        352 EQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKA 411
              |||| |||||||||||||||||||||||||      |||||||||         ||||
Db        310 EQKFGLEISPLCNQQKDSIPSIQIGFMSYIVEPALPGMAHFTGNSTLQRTCWATFAHNKG 369

Qy        412 QWKSLLPRQHRSRGSSGSGPDH 433
              |||||||    :  :    | ||
Db        370 QWKSLLPSSTEAGAALAXGLDH 391


RESULT 15
ADY50214
ID   ADY50214 standard; protein; 335 AA.
XX
AC   ADY50214;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human PDE7B phosphodiesterase domain SEQ ID NO:23.
XX
KW   phosphodiesterase 7B; PDE5A; X-ray crystallography; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2005048573-A1.
XX
PD   03-MAR-2005.
XX
PF   03-FEB-2004; 2004US-00771833.
XX
PR   03-FEB-2003; 2003US-0444734P.
PR   07-JUL-2003; 2003US-0485627P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Artis DR,  Bollag G,  Card G,  Martin F,  Milburn MV,  Zhang K;
XX
DR   WPI; 2005-202088/21.
XX
PT   Development of ligands binding to phosphodiesterase-5A (PDE5A) comprises
PT   identifying PDE5A binding compounds, determining orientation of molecular
PT   scaffold, identifying chemical structures of molecular scaffolds and
PT   synthesizing ligand.
XX
PS   Disclosure; SEQ ID NO 23; 111pp; English.
XX
CC   The invention relates to a novel method for development of ligands
CC   binding to phosphodiesterase-5A (PDE5A). The method comprises identifying
CC   one or more compounds as molecular scaffolds that bind to a binding site
CC   of PDE5A, determining the orientation of at least one molecular scaffold
CC   in co-crystals with PDE5A, identifying chemical structures of the
CC   molecular scaffolds, and synthesizing a ligand with altered binding
CC   affinity and/or binding specificity. The method to identify the potential
CC   PDE5A binding compounds comprises either removing a computer
CC   representation of a compound complexed with PDE5A or modifying a computer
CC   representation of a compound complexed with PDE5A by the deletion and/or
CC   addition of one or more chemical groups; fitting a computer
CC   representation of a compound from a computer database with a computer
CC   representation of the active site of PDE5A; and identifying compounds
CC   derived from the molecular scaffold that best fit the active site based
CC   on favorable geometric fit and energetically favorable complementary
CC   interactions as potential binding compounds; and further comprises
CC   searching a database for compounds having structural similarity to the
CC   molecular scaffold or derivative compound using a compound searching
CC   computer program or replacing portions of the compound with similar
CC   chemical structures using a compound construction computer program. The
CC   compound complexed with PDE5A is non-hydrolyzable cyclic guanosine
CC   monophosphate (cGMP) analog. The fitting comprises determining whether
CC   the compounds will interact with one or more of conserved PDE5A active
CC   site residues. The attachment component is a linker (a traceless linker)
CC   for attachment to a solid phase medium and comprises a label comprising a
CC   fluorophore. The attachment method further comprises attaching the
CC   compound or derivative to a solid phase medium through a linker attached
CC   at the energetically allowed site. The phosphodiesterase comprises
CC   conserved residues matching at least one conserved PDE5A active site
CC   residues. The phosphodiesterase binding compound or derivative is
CC   synthesized on the linker attached to the solid phase medium. The
CC   plurality of the compounds or derivatives is synthesized in combinatorial
CC   synthesis. The attachment of the compounds to the solid phase medium
CC   provides an affinity medium. The present sequence represents the
CC   phosphodiesterase domain of human phosphodiesterase 7B.
XX
SQ   Sequence 335 AA;

  Query Match           74.8%;  Score 1801;  DB 9;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-167;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 60
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Qy        147 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 120

Qy        207 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 180

Qy        267 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 240

Qy        327 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 300

Qy        387 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 421
              |||||||||||||||||||||||||||||||||||
Db        301 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 335
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Search completed: March 10, 2006, 19:56:52
Job time : 167.463 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:57:15 ; Search time 31.0976 Seconds
(without alignments)
1392.313 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2408 | 100.0 | 450 | 2 | JC7266 | 3',5'-cyclic-nucle |
| 2 | 1419.5 | 58.9 | 498 | 2 | A47286 | 3',5'-cyclic-AMP p |
| 3 | 604.5 | 25.1 | 673 | 2 | I61358 | 3',5'-cyclic-nucle |
| 4 | 603.5 | 25.1 | 584 | 2 | B53109 | 3',5'-cyclic-nucle |
| 5 | 603.5 | 25.1 | 672 | 2 | I61259 | 3',5'-cyclic-nucle |
| 6 | 580.5 | 24.1 | 562 | 2 | I59143 | cAMP phosphodieste |
| 7 | 580.5 | 24.1 | 564 | 2 | A40949 | cyclic-AMP phospho |
| 8 | 567.5 | 23.6 | 564 | 2 | JC1519 | 3',5'-cyclic-nucle |
| 9 | 567.5 | 23.6 | 736 | 2 | I61354 | phosphodiesterase |
| 10 | 565 | 23.5 | 886 | 2 | A54442 | 3',5'-cyclic-nucle |
| 11 | 559.5 | 23.2 | 610 | 2 | I67946 | 3',5'-cyclic-nucle |
| 12 | 559.5 | 23.2 | 844 | 2 | I53865 | phosphodiesterase |
| 13 | 553 | 23.0 | 712 | 2 | S71626 | 3',5'-cyclic-nucle |
| 14 | 529.5 | 22.0 | 536 | 2 | I67945 | 3',5'-cyclic-nucle |
| 15 | 517 | 21.5 | 549 | 2 | T16769 | hypothetical prote |
| 16 | 493 | 20.5 | 777 | 2 | S65543 | 3',5'-cyclic-nucle |
| 17 | 477.5 | 19.8 | 323 | 2 | S55348 | 3',5'-cyclic-nucle |
| 18 | 468 | 19.4 | 267 | 2 | B33904 | cAMP phosphodieste |
| 19 | 468 | 19.4 | 535 | 1 | A46378 | 3',5'-cyclic-nucle |
| 20 | 467 | 19.4 | 534 | 1 | A44162 | 3',5'-cyclic-nucle |
| 21 | 466 | 19.4 | 519 | 2 | T14783 | hypothetical prote |
| 22 | 466 | 19.4 | 535 | 1 | A44161 | 3',5'-cyclic-nucle |
| 23 | 461 | 19.1 | 664 | 2 | T24459 | hypothetical prote |
| 24 | 454.5 | 18.9 | 530 | 1 | A45334 | 3',5'-cyclic-nucle |
| 25 | 452.5 | 18.8 | 768 | 2 | T10796 | 3',5'-cyclic-nucle |
| 26 | 449 | 18.6 | 536 | 1 | JC6129 | 3',5'-cyclic-nucle |
| 27 | 445.5 | 18.5 | 713 | 2 | JW0088 | 3',5'-cyclic-nucle |
| 28 | 441 | 18.3 | 659 | 2 | JE0293 | 3',5'-cyclic-nucle |
| 29 | 441 | 18.3 | 885 | 2 | JC7898 | 3',5'-cyclic nucle |
| 30 | 409 | 17.0 | 491 | 2 | A40283 | 3',5'-cyclic-nucle |
| 31 | 381 | 15.8 | 875 | 1 | JW0106 | 3',5'-cyclic-GMP p |
| 32 | 377 | 15.7 | 875 | 1 | A48719 | 3',5'-cyclic-GMP p |
| 33 | 370 | 15.4 | 1054 | 2 | T30901 | cyclic nucleotide |
| 34 | 368.5 | 15.3 | 1112 | 2 | S70522 | cyclic nucleotide |
| 35 | 357.5 | 14.8 | 1108 | 2 | A48508 | cyclic-nucleotide |
| 36 | 346 | 14.4 | 1141 | 2 | A44093 | cGMP-inhibited cAM |
| 37 | 302.5 | 12.6 | 858 | 2 | JC4520 | 3',5'-cyclic-GMP p |
| 38 | 300 | 12.5 | 855 | 2 | A34810 | 3',5'-cyclic-GMP p |
| 39 | 299 | 12.4 | 928 | 1 | JC2486 | 3',5'-cyclic-nucle |
| 40 | 296 | 12.3 | 921 | 1 | A40981 | 3',5'-cyclic-nucle |
| 41 | 283 | 11.8 | 853 | 2 | A36617 | 3',5'-cyclic-GMP p |
| 42 | 279 | 11.6 | 856 | 1 | A47451 | 3',5'-cyclic-GMP p |
| 43 | 278 | 11.5 | 856 | 2 | S30762 | 3',5'-cyclic-GMP p |
| 44 | 277.5 | 11.5 | 854 | 2 | A42828 | 3',5'-cyclic-GMP p |
| 45 | 269.5 | 11.2 | 862 | 2 | I50186 | 3',5'-cyclic-GMP p |

ALIGNMENTS

RESULT 1
JC7266
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human
N;Alternate names: cAMP-specific phosphodiesterase 7B
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7266
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.
Biochem. Biophys. Res. Commun. 271, 575-583, 2000
A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.
A;Reference number: JC7266
A;Accession: JC7266
A;Molecule type: mRNA
A;Residues: 1-450 <SAS>
A;Cross-references: UNIPROT:Q9NP56; UNIPARC:UPI00000339FF; DDBJ:AB038040
A;Experimental source: caudate nucleus
C;Genetics:
A;Gene: pde7B
A;Map position: 6q23-24
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: phosphoric diester hydrolase

Query Match 100.0%; Score 2408; DB 2; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.4e-182;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
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Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 2
A47286
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000
C;Accession: A47286
R;Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers
J. Biol. Chem. 268, 12925-12932, 1993
A;Title: Isolation and characterization of a previously undetected human cAMP phosphodie
A;Reference number: A47286; MUID:93286141; PMID:8389765
A;Accession: A47286
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-498 <MIC>
A;Cross-references: UNIPARC:UPI00001440E6; GB:L12052; NID:g179892; PID:g179893
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             58.9%;  Score 1419.5;  DB 2;  Length 498;
  Best Local Similarity   61.7%;  Pred. No. 5e-104;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||      |::||:|| |||: || ||| |:||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:||||||||||||||||||||||
Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:||||||:||||:|:  ::||   || ||
Db        302 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 361

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:|||||||||||| ||:|||||:| |||: ||::|:|: | :||||::
Db        362 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 421

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:||||| ||| |: |: ||: ||||:  ||| || |   |  |  :
Db        422 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 480

Qy        427 SGS 429
              :
Db        481 DAA 483


RESULT 3
I61358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human
N;Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: I61358; I38416
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61358
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-673 <RES>
A;Cross-references: UNIPARC:UPI0000050EB5; GB:L20970; NID:g347129; PIDN:AAA03592.1; PID:g
R;Baecker, P.A.; Obernolte, R.; Bach, C.; Yee, C.; Shelton, E.R.
Gene 138, 253-256, 1994
A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodieste
A;Reference number: I38416; MUID:94171048; PMID:8125310
A;Accession: I38416
A;Molecule type: mRNA
A;Residues: 70-507,'P',509-673 <RE2>
A;Cross-references: UNIPARC:UPI000016A067; EMBL:U02882; NID:g433346; PIDN:AAC13745.1; PID
C;Genetics:
A;Gene: GDB:PDE4D; DPDE3
A;Cross-references: GDB:132541; OMIM:600129
A;Map position: 5q12-5q12
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

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Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:   ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 610


RESULT 4
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B53109; A34414; C33904; I67944
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP ph
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: B53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <MON>
A;Cross-references: UNIPROT:P14270; UNIPARC:UPI000002A6E1; GB:U01280
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A;Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormone
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A;Reference number: A34414; MUID:90046763; PMID:2554303
A;Accession: A34414
A;Molecule type: mRNA
A;Residues: 1-584 <SWI>
A;Cross-references: UNIPARC:UPI000002A6E1; GB:U09455; GB:M25349; NID:g517501; PIDN:AAA20
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: C33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 214-480 <SW2>
A;Cross-references: UNIPARC:UPI00001759B1; GB:M25349
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67944
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'EFPGES',34-421,'E',423-584 <RES>
A;Cross-references: UNIPARC:UPI00001759B2; GB:L27060; NID:g436009; PID:g436010
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative initiators; alternative splicing; cAMP binding; phosphoric diest
F;237-465/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             25.1%;  Score 603.5;  DB 2;  Length 584;
  Best Local Similarity   33.3%;  Pred. No. 1.2e-39;
  Matches  135;  Conservative   85;  Mismatches  152;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        130 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 186

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :|||
Db        187 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 245

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        246 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 305

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :    ::||||:::    |  ||  :
Db        306 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMV 365

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        366 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 425

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        426 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 483

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |:|:|
Db        484 YQSTIPQ------SPSPAPDDQEDGRQGQTEKFQFELTLEEDGES 522


RESULT 5
I61259
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form P
N;Alternate names: cyclic-AMP phosphodiesterase
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, s
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000
C;Accession: I61259; A53678; I67943
R;Sette, C.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 18271-18274, 1994
A;Title: The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins differential
A;Reference number: A53678; MUID:94308045; PMID:8034568
A;Accession: I61259
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-672 <RES>
A;Cross-references: UNIPARC:UPI00001759B7; EMBL:U09457; NID:g517418; PID:g517419
A;Accession: A53678
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 167-672 <RE2>
A;Cross-references: UNIPARC:UPI00001707C8; EMBL:U09456; NID:g517416; PIDN:AAA20393.1; PID
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67943
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'N',96-625,'Y',627-672 <RE3>
A;Cross-references: UNIPARC:UPI0000170BF4; GB:L27059; NID:g436007; PIDN:AAA56857.1; PID:g
C;Genetics:
A;Gene: PDE3/IVd gene
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             25.1%;  Score 603.5;  DB 2;  Length 672;
  Best Local Similarity   33.3%;  Pred. No. 1.5e-39;
  Matches  135;  Conservative   85;  Mismatches  152;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :|||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :    ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |:|:|
Db        572 YQSTIPQ------SPSPAPDDQEDGRQGQTEKFQFELTLEEDGES 610


RESULT 6
I59143
cAMP phosphodiesterase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59143
R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A;Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAMP
A;Reference number: I59143; MUID:89264471; PMID:2542941
A;Accession: I59143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-562 <RES>
A;Cross-references: UNIPROT:P14646; UNIPARC:UPI00001440E1; GB:J04563; NID:g203967; PIDN:A
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
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F;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 562;
Best Local Similarity 31.9%; Pred. No. 7.7e-38;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

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Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               ||| ::|::     ::  |:| |     | :  ::  :||:| :    |:|   | :||
Db         124 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 180

Qy         122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                 ::   |  ::  :|    |:  ||:   |   ::: ::: |||   |||::|||||
Db         181 VAGYSHNRPLTCIMYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADV 240

Qy         182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
               |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db         241 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 300

Qy         242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
               |||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         301 LENHHLAVGFKLLQEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 360

Qy         300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
               |       | |::  ||  :|:  : |||: || :  |: :||::|: |||::||: |:
Db         361 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 420

Qy         354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
               :  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:  :
Db         421 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 478

Qy         414 KSLLPR------QHRSRGSSGSGPDHDH----AGQGTESEEQEGDSP 450
               :|::|:        |||   |              : :|  |:||: |
Db         479 QSMIPQSPSPPLDERSRDCQGLMEKFQFELTLEEEDSEGPEKEGEGP 525
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RESULT 7
A40949
cyclic-AMP phosphodiesterase (EC 3.1.4.-) - rat
N;Alternate names: PDE4/IVb long form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jul-2004
C;Accession: A40949; D33904; A53109; I67942
R;Swinnen, J.V.; Tsikalas, K.E.; Conti, M.
J. Biol. Chem. 266, 18370-18377, 1991
A;Title: Properties and hormonal regulation of two structurally related cAMP phosphodies
A;Reference number: A40949; MUID:92011578; PMID:1655746
A;Accession: A40949
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <SWI>
A;Cross-references: UNIPROT:P14646; UNIPARC:UPI000002A6D9; GB:M25350
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: D33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 210-476 <SW2>
A;Cross-references: UNIPARC:UPI00001759B3; GB:M25350
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: A53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358,'S',360-564 <MON>
A;Cross-references: UNIPARC:UPI0000170820; GB:U01291; NID:g409826; PIDN:AAA18926.1; PID:
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996

A;Accession: I67942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: UNIPARC:UPI000002A6D9; GB:L27058; NID:g950096; PIDN:AAA74478.1; PID:g
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 580.5; DB 2; Length 564;
Best Local Similarity 31.9%; Pred. No. 7.7e-38;
Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

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Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               ||| ::|::     ::  |:| |     | :  ::  :||:| :    |:|   | :||
Db         126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 182

Qy         122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                 ::   |  ::  :|    |:  ||:   |   ::: ::: |||   |||::|||||
Db         183 VAGYSHNRPLTCIMYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADV 242

Qy         182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
               |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db         243 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 302

Qy         242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
               |||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         303 LENHHLAVGFKLLQEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 362

Qy         300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
               |       | |::  ||  :|:  : |||: || :  |: :||::|: |||::||: |:
Db         363 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 422

Qy         354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
               :  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:  :
Db         423 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 480

Qy         414 KSLLPR------QHRSRGSSGSGPDHDH----AGQGTESEEQEGDSP 450
               :|::|:        |||   |              : :|  |:||: |
Db         481 QSMIPQSPSPPLDERSRDCQGLMEKFQFELTLEEEDSEGPEKEGEGP 527
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RESULT 8
JC1519
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBP106) - h
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JC1519; A45500; I61359
R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, K.
Gene 129, 239-247, 1993
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a n
A;Reference number: JC1519; MUID:93314968; PMID:8392015
A;Accession: JC1519
A;Molecule type: mRNA
A;Residues: 1-564 <OBE>
A;Cross-references: UNIPROT:Q13945; UNIPARC:UPI000014C5AB; GB:L12686
A;Experimental source: lymphocyte
A;Note: only partial nucleotide sequence is given
R;McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.
J. Biol. Chem. 268, 6470-6476, 1993
A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain.
f mRNA.
A;Reference number: A45500; MUID:93203241; PMID:8384210
A;Accession: A45500
A;Molecule type: mRNA
A;Residues: 1-564 <MCL>
A;Cross-references: UNIPARC:UPI000014C5AB; GB:M97515; NID:g292387; PIDN:AAA36426.1; PID:g
A;Experimental source: frontal cortex
A;Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBIP:127930)
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory
A;Reference number: A54442; MUID:94019330; PMID:8413254

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A;Accession: I61359
A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: UNIPARC:UPI000014C5AB; GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             23.6%;  Score 567.5;  DB 2;  Length 564;
  Best Local Similarity   31.3%;  Pred. No. 8.1e-37;
  Matches  129;  Conservative   93;  Mismatches  149;  Indels   41;  Gaps    8;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |    | :  ::  :||:| :     |:|   | :||
Db        126 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 182

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||
Db        183 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 242

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
              |: | |  | | :  | |:|:  : ||| |||||||:  ||| ||  || :| : ||
Db        243 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 302

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
              |||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        303 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 362

Qy        300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
               |       | |::  ||  :|:  : |||: || :  |: :||::|: |||::||: |:
Db        363 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 422

Qy        354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
              :  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:  :
Db        423 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 480

Qy        414 KSLLPRQHRSRGSSGSGP----DHDHAG------------QGTESEEQEGD 448
              :|::|:       | | |    : |  |             : :|  |:||:
Db        481 QSMIPQ-------SPSPPLDEQNRDCQGLMEKFQFELTLDEEDSEGPEKEGE 525


RESULT 9
I61354
phosphodiesterase - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I61354
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61354
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-736 <RES>
A;Cross-references: UNIPROT:Q07343; UNIPARC:UPI0000127BF6; GB:L20966; NID:g347121; PIDN:
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             23.6%;  Score 567.5;  DB 2;  Length 736;
  Best Local Similarity   31.3%;  Pred. No. 1.2e-36;
  Matches  129;  Conservative   93;  Mismatches  149;  Indels   41;  Gaps    8;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::      ::  |:| |    | :  ::  :||:| :     |:|   | :||
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Db        355 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 414

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
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Db        415 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 474

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
              |||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        475 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 534

Qy        300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
               |       | |::  ||  :|:  : |||: || :  |: :||::|: |||::||: |:
Db        535 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 594

Qy        354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
              :  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:  :
Db        595 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 652

Qy        414 KSLLPRQHRSRGSSGSGP----DHDHAG------------QGTESEEQEGD 448
              :|::|:       | | |    : |  |             : :|  |:||:
Db        653 QSMIPQ-------SPSPPLDEQNRDCQGLMEKFQFELTLDEEDSEGPEKEGE 697


RESULT 10
A54442
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice fo
N;Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A54442; S55788; A36317; S55787
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, M
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memory
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: A54442
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-886 <RES>
A;Cross-references: UNIPROT:P27815; UNIPARC:UPI0000047003; GB:L20965; NID:g347119; PIDN:A
R;Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.
Cell. Signal. 6, 793-812, 1994
A;Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a hu
A;Reference number: S55788; MUID:95194817; PMID:7888306
A;Accession: S55788
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-735,'E',737-886 <SUL>
A;Cross-references: UNIPARC:UPI000002A6CE; EMBL:U18087; NID:g604374; PIDN:AAC50458.1; PID
A;Note: 736-Ala was also found
R;Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Davis
Mol. Cell. Biol. 10, 2678-2686, 1990
A;Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic AM
A;Reference number: A36317; MUID:90258854; PMID:2160582
A;Accession: A36317
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-516,'Y',518-722,'R',724-726,'R',728-735,'E',737-788,'E',790-7
A;Cross-references: UNIPARC:UPI000017C062; GB:M37744
C;Genetics:
A;Gene: GDB:PDE4A; DPDE2
A;Cross-references: GDB:138776; OMIM:600126
A;Map position: 19p13.1-19q12
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             23.5%;  Score 565;  DB 2;  Length 886;
  Best Local Similarity   32.1%;  Pred. No. 2.4e-36;
  Matches  126;  Conservative   82;  Mismatches  165;  Indels   20;  Gaps    6;

Qy         69 VKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNG 128
              : .:   ::  |:: |    ||:  :    |: | |    |:|   |  :||       |
Db        332 MSQITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQELENLNK---WGLNIFCVSDYAGG 388

Qy        129 NSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCY 188
              ||  ::  :|    |:  |:: : |:  ::: ::: ||:   |||::|||||  |: |
Db        389 RSLTCIMYMIFQERDLLKKFRIPVDTMVTYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 448
```

```
Qy        189 LKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWR 248
Db        449 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 508

Qy        249 STIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKD---- 302
Db        509 VGFKLLQEDNCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 568

Qy        303 --LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
Db        569 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 628

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLL--- 417
Db        629 PMCDKHTASVEKSQVGFIDYIVHPLWETWADLVHPD--AQEILDTLEDNRDWYYSAIRQS 686

Qy        418 ---PRQHRSRGSSGSG-PDHDHAGQGTESEEQE 446
Db        687 PSPPPEEESRGPGHPPLPDKFQFELTLEEEEEE 719
```

RESULT 11
I67946
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N;Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67946; A32558; B32558; C32558
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67946
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-610 <RES>
A;Cross-references: UNIPROT:P54748; UNIPARC:UPI000002A6D4; GB:L27062; NID:g436013; PIDN:
R;Davis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A;Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+) g
A;Reference number: A32558; MUID:89264472; PMID:2542942
A;Accession: A32558
A;Molecule type: mRNA
A;Residues: 1-598,'T',600-610 <DAV>
A;Cross-references: UNIPARC:UPI0000170937; GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:
A;Accession: B32558
A;Molecule type: mRNA
A;Residues: 85-120,154-598,'T',600-610 <DA2>
A;Cross-references: UNIPARC:UPI0000170939; GB:M26716; GB:M26717; GB:J04554; NID:g203986;
A;Note: splice form RD2
A;Accession: C32558
A;Molecule type: mRNA
A;Residues: 26-598,'T',600-610 <DA3>
A;Cross-references: UNIPARC:UPI0000170938; GB:M26716; NID:g203984; PIDN:AAA41101.1; PID:
A;Note: splice form RD3
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;14-20/Region: responsible for membrane association
F;26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pr
F;85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 #s
F;184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             23.2%;  Score 559.5;  DB 2;  Length 610;
  Best Local Similarity   31.1%;  Pred. No. 3.9e-36;
  Matches  133;  Conservative   77;  Mismatches  163;  Indels   55;  Gaps    9;

```
Qy         43 RGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYL 102
Db         80 RQSQPMSQITGLKKLVHTGSLNTN----------------------VPRFGVKTDQEDLL 117

Qy        103 GQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMV 162
Db        118 AQELENLSK---WGLNIFCVSEYAGGRSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTL 174

Qy        163 QEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQ 222
Db        175 EDHYHADVAYHNSLHAADVLQSTHVLLATPALDAVFTDLEILAALFAAAIHDVDHPGVSN 234

Qy        223 PFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLIL 280
Db        235 QFLINTNSELALMYNDESVLENHHLAVGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVL 294

Qy        281 ATDINRQNEFLTRLKAHLHNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMS 334
Db        295 ATDMSKHMTLLADLKTMVETKKVTSSGVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELY 354

Qy        335 KQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTG 394
Db        355 RQWTDRIMAEFFQQGDRERERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVH 414

Qy        395 NSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGP-DHDHAGQG------------TE 441
Db        415 PD--AQDILDTLEDNR-DW------YHSAIRQSPSPPLEEEPGGLGHPSLPDKFQFELTL 465

Qy        442 SEEQEGDS 449
Db        466 EEEEEEDS 473
```

RESULT 12
I53865
phosphodiesterase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I53865
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I53865
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-844 <RES>
A;Cross-references: UNIPROT:P54748; UNIPARC:UPI0000127BF5; GB:L27057; NID:g3334904; PIDN:
F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             23.2%;  Score 559.5;  DB 2;  Length 844;
  Best Local Similarity   31.1%;  Pred. No. 6e-36;
  Matches  133;  Conservative   77;  Mismatches  163;  Indels   55;  Gaps    9;

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Qy         43 RGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYL 102
Db        314 RQSQPMSQITGLKKLVHTGSLNTN----------------------VPRFGVKTDQEDLL 351

Qy        103 GQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMV 162
Db        352 AQELENLSK---WGLNIFCVSEYAGGRSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTL 408

Qy        163 QEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQ 222
Db        409 EDHYHADVAYHNSLHAADVLQSTHVLLATPALDAVFTDLEILAALFAAAIHDVDHPGVSN 468

Qy        223 PFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLIL 280
Db        469 QFLINTNSELALMYNDESVLENHHLAVGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVL 528

Qy        281 ATDINRQNEFLTRLKAHLHNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMS 334
Db        529 ATDMSKHMTLLADLKTMVETKKVTSSGVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELY 588

Qy        335 KQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTG 394
Db        589 RQWTDRIMAEFFQQGDRERERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVH 648
```

```
Qy        395 NSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGP-DHDHAGQG------------TE 441
              ::::|  |  |:  |       | :  | | | : :  | |             |
Db        649 PD--AQDILDTLEDNR-DW------YHSAIRQSPSPPLEEEPGGLGHPSLPDKFQFELTL 699

Qy        442 SEEQEGDS 449
              ||:| ||
Db        700 EEEEEEDS 707


RESULT 13
S71626
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71626; I61356
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.
FEBS Lett. 358, 305-310, 1995
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific p
A;Reference number: S71626; MUID:95145731; PMID:7843419
A;Accession: S71626
A;Molecule type: DNA
A;Residues: 1-712 <ENG>
A;Cross-references: UNIPROT:Q08493; UNIPARC:UPI0000163B31; EMBL:Z46632; NID:g727222; PID
A;Experimental source: substantia nigra
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61356
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 462-712 <RES>
A;Cross-references: UNIPARC:UPI000016AE86; GB:L20968; NID:g347125; PIDN:AAA03591.1; PID:
C;Genetics:
A;Gene: HSPDE4C1
C;Function:
A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP
A;Pathway: cyclic nucleotide metabolism
A;Note: expressed in various tissues but not in cells of the immune system
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match            23.0%;  Score 553;  DB 2;  Length 712;
  Best Local Similarity  27.8%;  Pred. No. 1.6e-35;
  Matches  135;  Conservative   94;  Mismatches  198;  Indels   58;  Gaps   10;

Qy         11 EILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLN-------STTYSG-- 61
              ::  |  |:   |:  |  :: |   |  |  :        |:||       |: ||
Db        204 KLALETLDELDWCLDQLETLQTRHSVGEMASNKFK------RILNRELTHLSETSRSGNQ 257

Qy         62 --------------EIGTKK--------KVKRLLSFQRYFHASRLLRGIIPQAPLHLLDE 99
                           |:   |         : |:       |:: |    :|:  :    |
Db        258 VSEYISRTFLDQQTEVELPKVTAEEAPQPMSRISGLHGLCHSASLSSATVPRFGVQTDQE 317

Qy        100 DYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFL 159
              : | :    |     |  |:|    ::    |  ::  :|    |:  |::   ||  :|
Db        318 EQLAKE---LEDTNKWGLDVFKVADVSGNRPLTAIIFSIFQERDLLKTFQIPADTLATYL 374

Qy        160 VMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPG 219
              :|::  ||:   |||::|||| |: |  |  | :  | |:|:  | |:| |||||||
Db        375 LMLEGHYHANVAYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALFASAIHDVDHPG 434

Qy        220 VNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGS 277
              |:  ||| ||  :| :| : |||||||      :|:     :  :|  :    : : :
Db        435 VSNQFLINTNSDVALMYNDASVLENHHLAVGFKLLQAENCDIFQNLSAKQRLSLRRMVID 494

Qy        278 LILATDINRQNEFLTRLKAHLHNKD------LRLEDAQDRHFMLQIALKCADICNPCRIW 331
              ::||||:::    |  ||  :  |       | |::  ||  :||  : |||: || :
Db        495 MVLATDMSKHMNLLADLKTMVETKKVTSLGVLLLDNYSDRIQVLQNLVHCADLSNPTKPL 554

Qy        332 EMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAH 391
```

```
Db        555 PLYRQWTDRIMAEFFQQGDRERESGLDISPMCDKHTASVEKSQVGFIDYIAHPLWETWAD 614

Qy        392 FTGNSTLSENMLGHLAHNKAQWKSLLPRQHRS-RGSSGSGPDH-------DHAGQGTESE 443
              ::::|  |  |:  ::| :||           |||        : | :  | |
Db        615 LVHPD--AQDLLDTLEDNREWYQSKIPRSPSDLTNPERDGPDRFQFELTLEEAEEEDEEE 672

Qy        444 EQEGD 448
              |:||:
Db        673 EEEGE 677


RESULT 14
I67945
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)
N;Alternate names: cAMP phosphodiesterase 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67945; A33904
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67945
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-536 <RES>
A;Cross-references: UNIPROT:P14644; UNIPARC:UPI0000127BF9; GB:L27061; NID:g436011; PIDN:A
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP ph
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: A33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 230-496 <SWI>
A;Cross-references: UNIPARC:UPI00001759B4; GB:M25347; GB:M28410
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;253-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

  Query Match            22.0%;  Score 529.5;  DB 2;  Length 536;
  Best Local Similarity  30.8%;  Pred. No. 7.5e-34;
  Matches  120;  Conservative   79;  Mismatches  169;  Indels   21;  Gaps    7;

Qy         71 RLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNS 130
              ::   ::  | | |    ||:  :    |: | :    |      |  |:|    |:
Db        156 QITGLRKSCHTS-LPTAAIPRFGVQTDQEEQLAKE---LEDTNKWGLDVFKVAELSGNRP 211

Qy        131 LVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLK 190
              |  ::  :     |:  |::   || |:|: ::  |||   |||::|||| |: |  |
Db        212 LTAVIPRVLQERDLLKTFQIPADTLLRYLLTLEGHYHSNVAYHNSIHAADVVQSAHVLLG 271

Qy        191 EPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRST 250
              | | :  | |::  :  | | |||||||||:  ||| ||  || :| : |||||||
Db        272 TPALEAVFTDLEVLAAIFACAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVG 331

Qy        251 IGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKD------ 302
              :|:     :  :|  :    : : :  ::||||:::    |  ||  :  |
Db        332 FKLLQGENCDIFQNLSTKQKLSLRRMVIDMVLATDMSKHMSLLADLKTMVETKKVTSLGV 391

Qy        303 LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPL 362
              | |::  ||  :||  : |||: || :   : :||:||:  ||::||: |::  |:|||:
Db        392 LLLDNYSDRIQVLQSLVHCADLSNPAKPLPLYRQWTERIMAEFFQQGDRERESGLDISPM 451

Qy        363 CNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHR 422
              |::    |:   |:||: ||  ||:  ||          :: :|  |  |:  ::| :|
Db        452 CDKHTASVEKSQVGFIDYIAHPLWETWADLVHPD--AQELLDTLEDNREWYQSRVP---- 505

Qy        423 SRGSSGSGPDH---DHAGQGTESEEQEGD 448
                    |||    :   : || ||:| :
Db        506 CSPPHAIGPDRFKFELTLEETEEEEEEDE 534
```

RESULT 15
T16769
hypothetical protein R153.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16769
R;Kirsten, J.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid R153.
A;Reference number: Z18573
A;Accession: T16769
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-549 <KIR>
A;Cross-references: UNIPROT:Q22000; UNIPARC:UPI000013C0D8; EMBL:U28729; NID:g861238; PID
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:R153.1
A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 21.5%; Score 517; DB 2; Length 549;
Best Local Similarity 32.6%; Pred. No. 7.5e-33;
Matches 114; Conservative 72; Mismatches 140; Indels 24; Gaps 6;

```
Qy        105 ARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQE 164
              | ||  ::  |  |:|  | |:  :||  :   |     |   |::   ||  :|: ::
Db        216 AVHM-QRLDDWGPDVFKIDELSKNHSLTVVTFSLLRQRNLFKTFEIHQSTLVTYLLNLEH 274

Qy        165 DYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPF 224
              | : | ||| :||||| |:||  |  | |     | |:::  : | | |||||||    :
Db        275 HYRN-NHYHNFIHAADVAQSMHVLLMSPVLTEVFTDLEVLAAIFAGAVHDVDHPGFTNQY 333

Qy        225 LIKTNHHLANLYQNMSVLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILAT 282
              || :|: || :| : |||| ||      :|::|    ||:| ::      : :  ::|||
Db        334 LINSNNELAIMYNDESVLEQHHLAVAFKLLQDSNCDFLANLSRKQRLQFRKIVIDMVLAT 393

Qy        283 DINRQNEFLTRLKAHLH------NKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQ 336
              |:::    |  ||  :       |  : |:   |:  :||  :  ||: || :  |: :|
Db        394 DMSKHMSLLADLKTMVEAKKVAGNNVIVLDKYNDKIQVLQSMIHLADLSNPTKPIELYQQ 453

Qy        337 WSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNS 396
              |::|: ||::|||: |::  |||||:|::   :|   |:||: ||| ||:  ||
Db        454 WNQRIMEEYWRQGDKEKELGLEISPMCDRGNVTIEKSQVGFIDYIVHPLYETWADLVYPD 513

Qy        397 TLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQE 446
              ::|:|  |  |:  ::| :|            : | |   || :| :
Db        514 --AQNILDQLEENREWYQSRIPE----------EPDTARTVTEDDEHK 549
```

Search completed: March 10, 2006, 20:03:03
Job time : 32.0976 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 19:52:25 ; Search time 187.805 Seconds
(without alignments)
1690.519 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2408 | 100.0 | 450 | 1 | PDE7B_HUMAN | Q9np56 homo sapien |
| 2 | 2408 | 100.0 | 450 | 2 | Q5VWY9_HUMAN | Q5vwy9 homo sapien |
| 3 | 2258 | 93.8 | 586 | 2 | Q4LE81_HUMAN | Q4le81 homo sapien |
| 4 | 2192 | 91.0 | 446 | 1 | PDE7B_MOUSE | Q9qxq1 mus musculu |
| 5 | 2178 | 90.4 | 446 | 2 | Q8VIE4_RAT | Q8vie4 rattus norv |
| 6 | 2178 | 90.4 | 446 | 2 | Q8CBS2_MOUSE | Q8cbs2 mus musculu |
| 7 | 2161.5 | 89.8 | 459 | 2 | Q8VIE2_RAT | Q8vie2 rattus norv |
| 8 | 1764 | 73.3 | 359 | 2 | Q8VIE3_RAT | Q8vie3 rattus norv |
| 9 | 1510.5 | 62.7 | 456 | 2 | Q4RR95_TETNG | Q4rr95 tetraodon n |
| 10 | 1425.5 | 59.2 | 456 | 1 | PDE7A_MOUSE | P70453 mus musculu |
| 11 | 1424.5 | 59.2 | 482 | 2 | Q6P5G2_MOUSE | Q6p5g2 mus musculu |
| 12 | 1419.5 | 58.9 | 482 | 1 | PDE7A_HUMAN | Q13946 homo sapien |
| 13 | 1418.5 | 58.9 | 456 | 2 | Q5R5B5_PONPY | Q5r5b5 pongo pygma |
| 14 | 1397.5 | 58.0 | 426 | 1 | PDE7A_RAT | O08593 rattus norv |
| 15 | 1287 | 53.4 | 424 | 2 | Q96T72_HUMAN | Q96t72 homo sapien |
| 16 | 1267.5 | 52.6 | 381 | 2 | Q505M0_XENLA | Q505m0 xenopus lae |
| 17 | 1107.5 | 46.0 | 324 | 2 | Q4R6T4_MACFA | Q4r6t4 macaca fasc |
| 18 | 872 | 36.2 | 305 | 2 | Q7PNP5_ANOGA | Q7pnp5 anopheles g |
| 19 | 711 | 29.5 | 199 | 2 | Q4VXJ0_HUMAN | Q4vxj0 homo sapien |
| 20 | 604.5 | 25.1 | 809 | 1 | PDE4D_HUMAN | Q08499 homo sapien |
| 21 | 603.5 | 25.1 | 803 | 1 | PDE4D_RAT | P14270 rattus norv |
| 22 | 600.5 | 24.9 | 747 | 1 | PDE4D_MOUSE | Q01063 mus musculu |
| 23 | 580.5 | 24.1 | 659 | 2 | Q8VD81_RAT | Q8vd81 rattus norv |
| 24 | 580.5 | 24.1 | 721 | 1 | PDE4B_RAT | P14646 rattus norv |
| 25 | 580.5 | 24.1 | 722 | 2 | Q5RKL0_RAT | Q5rkl0 rattus norv |
| 26 | 580.5 | 24.1 | 736 | 2 | Q8VD82_RAT | Q8vd82 rattus norv |
| 27 | 579.5 | 24.1 | 691 | 2 | Q4RJ30_TETNG | Q4rj30 tetraodon n |
| 28 | 579 | 24.0 | 563 | 2 | Q5ZKR6_CHICK | Q5zkr6 gallus gall |
| 29 | 574.5 | 23.9 | 721 | 2 | Q9QXI7_MOUSE | Q9qxi7 mus musculu |
| 30 | 573.5 | 23.8 | 503 | 2 | Q6IQY6_MOUSE | Q6iqy6 mus musculu |
| 31 | 573.5 | 23.8 | 542 | 2 | Q91VY2_MOUSE | Q91vy2 mus musculu |
| 32 | 573.5 | 23.8 | 682 | 2 | Q5XGT5_XENLA | Q5xgt5 xenopus lae |
| 33 | 573.5 | 23.8 | 721 | 2 | Q8VBU5_MOUSE | Q8vbu5 mus musculu |
| 34 | 572 | 23.8 | 683 | 2 | Q4SBL4_TETNG | Q4sbl4 tetraodon n |
| 35 | 568 | 23.6 | 867 | 2 | Q4RL51_TETNG | Q4rl51 tetraodon n |
| 36 | 567.5 | 23.6 | 564 | 2 | Q5T3Z8_HUMAN | Q5t3z8 homo sapien |
| 37 | 567.5 | 23.6 | 606 | 2 | Q13945_HUMAN | Q13945 homo sapien |
| 38 | 567.5 | 23.6 | 721 | 2 | Q5VTH5_HUMAN | Q5vth5 homo sapien |
| 39 | 567.5 | 23.6 | 726 | 2 | Q59GM8_HUMAN | Q59gm8 homo sapien |
| 40 | 567.5 | 23.6 | 736 | 1 | PDE4B_HUMAN | Q07343 homo sapien |
| 41 | 567.5 | 23.6 | 736 | 2 | Q5VTH7_HUMAN | Q5vth7 homo sapien |
| 42 | 565 | 23.5 | 647 | 2 | Q8IVA7_HUMAN | Q8iva7 homo sapien |
| 43 | 565 | 23.5 | 825 | 2 | Q9H3H2_HUMAN | Q9h3h2 homo sapien |
| 44 | 565 | 23.5 | 860 | 2 | Q5DM53_HUMAN | Q5dm53 homo sapien |
| 45 | 565 | 23.5 | 864 | 2 | Q6PMT2_HUMAN | Q6pmt2 homo sapien |

ALIGNMENTS

RESULT 1
PDE7B_HUMAN
ID PDE7B_HUMAN STANDARD; PRT; 450 AA.
AC Q9NP56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN Name=PDE7B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20275458; PubMed=10814504; DOI=10.1006/bbrc.2000.2661;
RA Sasaki T., Kotera J., Yuasa K., Omori K.;
RT "Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT cAMP-specific nucleotide phosphodiesterase.";
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in the control of cAMP-mediated neural

```
CC       activity and cAMP metabolism in the brain.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed in
CC       heart, liver, skeletal muscle and pancreas.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB038040; BAA96537.1; -; mRNA.
DR   EMBL; AJ251860; CAB92441.1; -; mRNA.
DR   EMBL; BC075082; AAH75082.1; -; mRNA.
DR   EMBL; BC075083; AAH75083.1; -; mRNA.
DR   PIR; JC7266; JC7266.
DR   PDB; 1LXW; Model; A=104-433.
DR   Ensembl; ENSG00000171408; Homo sapiens.
DR   HGNC; HGNC:8792; PDE7B.
DR   MIM; 604645; -.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   3D-structure; cAMP; Hydrolase.
FT   REGION      172    410       Catalytic (By similarity).
SQ   SEQUENCE   450 AA;  51835 MW;  EC142BF3E28D0028 CRC64;

  Query Match           100.0%;  Score 2408;  DB 1;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-178;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 2
Q5VWY9_HUMAN
ID   Q5VWY9_HUMAN PRELIMINARY;      PRT;   450 AA.
AC   Q5VWY9;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   OTTHUMP00000017267.
GN   Name=PDE7B; ORFNames=RP11-472E5.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Thomas D.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Williams S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Cobley V.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL360178; CAH73075.1; -; Genomic_DNA.
DR   EMBL; AL138828; CAI95287.1; -; Genomic_DNA.
DR   EMBL; AL133319; CAH73332.1; -; Genomic_DNA.
DR   EMBL; AL133319; CAH73075.1; JOINED; Genomic_DNA.
DR   EMBL; AL138828; CAH73075.1; JOINED; Genomic_DNA.
DR   EMBL; AL138828; CAH73332.1; JOINED; Genomic_DNA.
DR   EMBL; AL133319; CAI95287.1; JOINED; Genomic_DNA.
DR   EMBL; AL360178; CAH73332.1; JOINED; Genomic_DNA.
DR   EMBL; AL360178; CAI95287.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000171408; Homo sapiens.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
SQ   SEQUENCE   450 AA;  51835 MW;  EC142BF3E28D0028 CRC64;

  Query Match           100.0%;  Score 2408;  DB 2;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-178;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
              |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 3
Q4LE81_HUMAN
ID   Q4LE81_HUMAN PRELIMINARY;      PRT;   586 AA.
AC   Q4LE81;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   PDE7B variant protein (Fragment).
GN   Name=PDE7B variant protein;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,
RA   Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;
RT   "Preparation of a set of expression-ready clones of mammalian long
RT   cDNAs encoding large proteins by the ORF trap cloning method.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB209990; BAE06072.1; -; mRNA.
FT   NON_TER       1       1
SQ   SEQUENCE   586 AA;  66230 MW;  F96F4F0549A9FE8D CRC64;

  Query Match             93.8%;  Score 2258;  DB 2;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 2e-166;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 223

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 283

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 343

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 403

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 463

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 523

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 583

Qy        448 DSP 450
              |||
Db        584 DSP 586


RESULT 4
PDE7B_MOUSE
ID   PDE7B_MOUSE    STANDARD;      PRT;   446 AA.
AC   Q9QXQ1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN   Name=Pde7b;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20087273; PubMed=10618442; DOI=10.1073/pnas.97.1.472;
RA   Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT   "Cloning and characterization of PDE7B, a cAMP-specific
RT   phosphodiesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20329226; PubMed=10872825; DOI=10.1006/bbrc.2000.2743;
RA   Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT   "Cloning and characterisation of the human and mouse PDE7B, a novel
RT   cAMP-specific nucleotide phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC   -!- FUNCTION: May be involved in the control of cAMP-mediated neural
CC       activity and cAMP metabolism in the brain.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF190639; AAF25195.1; -; mRNA.
DR   EMBL; AJ251859; CAB92530.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSMUSG00000019990; Mus musculus.
DR   MGI; MGI:1352752; Pde7b.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   cAMP; Hydrolase.
FT   REGION      172     410       Catalytic (By similarity).
SQ   SEQUENCE   446 AA;  51337 MW;  7C052664B693A5A8 CRC64;

  Query Match             91.0%;  Score 2192;  DB 1;  Length 446;
  Best Local Similarity   91.6%;  Pred. No. 1.9e-161;
  Matches  413;  Conservative   13;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
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Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Db        301 KDLRLENVQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Db        361 PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450

Db        421 HRRRGSG-----QDLAGPAPETLEQTEGATP 446
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RESULT 5
Q8VIE4_RAT
ID Q8VIE4_RAT PRELIMINARY; PRT; 446 AA.
AC Q8VIE4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17).
GN Name=Pde7b; Synonyms=RNPDE7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB057409; BAB79637.1; -; mRNA.
DR HSSP; Q08499; 1OYN.
DR Ensembl; ENSRNOG00000013436; Rattus norvegicus.
DR RGD; 621016; Pde7b.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 446 AA; 51475 MW; 01567BDABC905D19 CRC64;

Query Match 90.4%; Score 2178; DB 2; Length 446;
Best Local Similarity 90.7%; Pred. No. 2.3e-160;
Matches 409; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Db          1 MSCLMVERCGEVLFENPEQNVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Db         61 GEIGSKKKVRRLLSFQRHFHESRLLRGMTPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Db        301 KDLRLENIQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Db        361 PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSESMLNHLAHNKAQWKSLLSNQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450

Db        421 HRRRGSG-----QDPAGTAPETLEQTEGATP 446
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RESULT 6
Q8CBS2_MOUSE
ID Q8CBS2_MOUSE PRELIMINARY; PRT; 446 AA.
AC Q8CBS2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male urinary bladder cDNA, RIKEN full-length
DE enriched library, clone:9530027O16 product:phosphodiesterase 7B, full
DE insert sequence.
GN Name=Pde7b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK035385; BAC29052.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   MGI; MGI:1352752; Pde7b.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   446 AA;  51307 MW;  7C002364B396A5A8 CRC64;

  Query Match             90.4%;  Score 2178;  DB 2;  Length 446;
  Best Local Similarity   91.4%;  Pred. No. 2.3e-160;
  Matches  412;  Conservative   13;  Mismatches   20;  Indels    6;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              |||||||||||:|||:|:|: ||||||||:|||||||| |||||||||||||||||:||:|
Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||

Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||||:|||||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||: |||||||||||||||||||||||||||||||||||||||:||||||||||
Db        301 KDLRLENVQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              |||||||||||||||:||||||||| | |||||||||||| |||||||||||| |
Db        361 PLCNQQKDSIPSIQIGFMTYIVEPLFRERARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
              || |||       | ||   |: || || :|
Db        421 HRRRGSG-----QDLAGPAPETLEQTEGATP 446


RESULT 7
Q8VIE2_RAT
ID   Q8VIE2_RAT  PRELIMINARY;      PRT;   459 AA.
AC   Q8VIE2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).
GN   Name=Pde7b; Synonyms=RNPDE7B;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skeletal muscle;
RA   Sasaki T., Kotera J., Omori K.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057411; BAB79639.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSRNOG00000013436; Rattus norvegicus.
DR   RGD; 621016; Pde7b.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hydrolase.
SQ   SEQUENCE   459 AA;  52680 MW;  A3F26E95C7FC00A5 CRC64;

  Query Match             89.8%;  Score 2161.5;  DB 2;  Length 459;
  Best Local Similarity   88.1%;  Pred. No. 4.5e-159;
  Matches  409;  Conservative   16;  Mismatches   20;  Indels   19;  Gaps    3;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCML------------GDIRLRGQTGVRAERRGSYP 47
              |||||||||||:|||||:|| ||||||             ||:|||||||| ||||||||
Db          1 MSCLMVERCGEVLFENPEQNVKCVCMLAASSPPPLPMAGQGDVRLRGQTGVPAERRGSYP 60

Qy         48 FIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARH 107
              ||||||||:||:|||||:||||:|||||||:|| |||||: |||||||||||||||||||
Db         61 FIDFRLLNNTTHSGEIGSKKKVRRLLSFQRHFHESRLLRGMTPQAPLHLLDEDYLGQARH 120
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Qy        108 MLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYH 167
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 MLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYH 180

Qy        168 SQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIK 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIK 240

Qy        228 TNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQ 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQ 300

Qy        288 NEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYR 347
              ||||||||||||||||||: ||||||||||||||||||||||||||||||||||||||||
Db        301 NEFLTRLKAHLHNKDLRLENIQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYR 360

Qy        348 QGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLA 407
              ||:|||||||||||||||||||||||||:|||||||||| |||||||||:|| |||
Db        361 QGDLEQKFELEISPLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSESMLNHLA 420

Qy        408 HNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
              ||||||||||  ||| |||       | ||   |: || || :|
Db        421 HNKAQWKSLLSNQHRRRGSG-----QDPAGTAPETLEQTEGATP 459
```

RESULT 8
Q8VIE3_RAT
ID Q8VIE3_RAT PRELIMINARY; PRT; 359 AA.
AC Q8VIE3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B3 (EC 3.1.4.17).
GN Name=Pde7b; Synonyms=RNPDE7B;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Sasaki T., Kotera J., Omori K.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB057410; BAB79638.1; -; mRNA.
DR HSSP; Q08499; 1OYN.
DR RGD; 621016; Pde7b.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 359 AA; 41456 MW; 0FF72792737CE48A CRC64;

Query Match 73.3%; Score 1764; DB 2; Length 359;
Best Local Similarity 92.0%; Pred. No. 2.3e-128;
Matches 333; Conservative 7; Mismatches 16; Indels 6; Gaps 2;

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Qy         90 PQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFK 149
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db          3 PQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHHFK 62

Qy        150 LDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLA 209
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         63 LDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLA 122

Qy        210 AAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQ 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 AAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQ 182

Qy        270 DIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCR 329
              ||||||||||||||||||||||||||||||||||||||||: ||||||||||||||||||
Db        183 DIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENIQDRHFMLQIALKCADICNPCR 242

Qy        330 IWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREW 389
              ||||||||||||||||||:||||||||||||||||||||||||||:||||||||||
Db        243 IWEMSKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGFMTYIVEPLFREW 302

Qy        390 AHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQ-EGD 448
              | |||||||||:|| |||||||||||||  ||| |||       | ||   |: || ||
Db        303 ARFTGNSTLSESMLNHLAHNKAQWKSLLSNQHRRRGSG-----QDPAGTAPETLEQTEGA 357

Qy        449 SP 450
              :|
Db        358 TP 359
```

RESULT 9
Q4RR95_TETNG
ID Q4RR95_TETNG PRELIMINARY; PRT; 456 AA.
AC Q4RR95;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 14 SCAF15003, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00030267001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetradontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015003; CAG09087.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 456 456
SQ SEQUENCE 456 AA; 52118 MW; 60B4805381D70669 CRC64;

Query Match 62.7%; Score 1510.5; DB 2; Length 456;
Best Local Similarity 64.5%; Pred. No. 1.4e-108;
Matches 294; Conservative 52; Mismatches 63; Indels 47; Gaps 8;

```
Qy          7 ERCGEILFENPDQNAKCVCML----------------GDIRL-RGQTGV-RAERRGSYP 47
              :||| :   :|:|||  | ||                : :|  |  ||   |||||||
Db          1 QRCGAVTLTSPEQNAVQVRMLDRHVDRNRPKHLPAASIAECKLSTGHAGVLLVERRGSYP 60
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```
Qy          48 FIDFRLLNSTTYSGEI--GTKKKVKRLLSFQRYFHASRLLRGIIPQAP--LHLLDEDYLG 103
               || ::| |::  ||:  ||::||:| |||||| |||||||::| ||  |||||: |||
Db          61 LIDLQVLKSSSQQGEVASGTRRKVQRQLSFQRYCHASRLLRGLVPHAPLSLHLLDDGYLG 120

Qy         104 QARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQ 163
               || ||||||| |:||||||||||||||||||:||||| :||:|||:|||| ||||| |||
Db         121 QAAHMLSKVGTWNFDIFLFDRLTNGNSLVTLMCHLFNVYGLVHHFQLDMVKLHRFLGMVQ 180

Qy         164 EDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQP 223
               |||||||||||||||||||:|||||||||  |:|||: |||:|||||||||||||||||
Db         181 EDYHSQNPYHNAVHAADVTQAMYCYLKEPKLAEQLSPLDVFLGLMAAAAHDVDHPGVNQP 240

Qy         224 FLIKTNHHLANLY------QNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGS 277
               ||||| ||||:||      || ||||:||||||:|||||| ||:||| :|:|||||||||
Db         241 FLIKTRHHLASLYQVHQSVQNTSVLESHHWRSTVGMLRESGLLSHLPADMSQDIEQQLGS 300

Qy         278 LILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFML----------------QIALK 320
               |||||||:||||||     || ::|| |:    |||:|                |||||
Db         301 LILATDISRQNEFLLTFGEHLDHQDLDLQLPSHRHFILQHAFRRSVPAVTACVCQQIALK 360

Qy         321 CADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSY 380
               |||:|||||:| :|:|||||||||:|||:||:||:|||||||: ::   |:|| ||:||
Db         361 CADVCNPCRVWALSRQWSERVCEEFFRQGDLERKFDLEISPLCDSRR-LRPAIQTGFISY 419

Qy         381 IVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSL 416
               |||||| ||  ||  | ||  |:|||  |||:|  |
Db         420 IVEPLFDEWHRFTEPSPLSRTMMGHLHQNKARWSRL 455
```

RESULT 10
PDE7A_MOUSE
ID PDE7A_MOUSE STANDARD; PRT; 456 AA.
AC P70453; Q9ERB3;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE (EC 3.1.4.17) (P2A).
GN Name=Pde7a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Skeletal muscle;
RX MEDLINE=97098542; PubMed=8943082; DOI=10.1073/pnas.93.24.14188;
RA Bloom T.J., Beavo J.A.;
RT "Identification and tissue-specific expression of PDE7
RT phosphodiesterase splice variants.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Brain, and Testis;
RX MEDLINE=20483661; PubMed=11027622; DOI=10.1006/bbrc.2000.3613;
RA Wang P., Wu P., Egan R.W., Billah M.M.;
RT "Cloning, characterization, and tissue distribution of mouse
RT phosphodiesterase 7A1.";
RL Biochem. Biophys. Res. Commun. 276:1271-1277(2000).
CC -!- FUNCTION: Plays a role in signal transduction by regulating the
CC intracellular concentration of cyclic nucleotides. This
CC phosphodiesterase is highly specific for cAMP and may have a role
CC in muscle signal transduction.
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC adenosine 5'-phosphate.
CC -!- COFACTOR: Divalent cations.
CC -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=PDE7A2;
CC IsoId=P70453-1; Sequence=Displayed;
CC Name=2; Synonyms=PDE7A1;
CC IsoId=P70453-2; Sequence=VSP_004594;
CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in the
CC skeletal muscle.
CC -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC putative divalent metal sites and an N-terminal regulatory domain.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC ----------------------------------------------------------------------
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ----------------------------------------------------------------------
DR EMBL; U68171; AAB08479.1; -; mRNA.
DR EMBL; AY007702; AAG16295.1; -; mRNA.
DR HSSP; Q08499; 1OYN.
DR Ensembl; ENSMUSG00000019990; Mus musculus.
DR MGI; MGI:1202402; Pde7a.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Alternative splicing; cAMP; Hydrolase.
FT REGION 161 425 Catalytic (By similarity).
FT VARSPLIC 1 20 MGITLIWCLALVLIKWITSK -> MEVCYQLPVLPLDRPVP
FT QHVLSRRGAISFSSSSALFGCPHPRQLSQ (in isoform
FT 2).
FT /FTId=VSP_004594.
FT CONFLICT 407 407 A -> D (in Ref. 2).
SQ SEQUENCE 456 AA; 52442 MW; 0B826B96490D9F6E CRC64;

Query Match 59.2%; Score 1425.5; DB 1; Length 456;
Best Local Similarity 62.2%; Pred. No. 5.7e-102;
Matches 263; Conservative 71; Mismatches 88; Indels 1; Gaps 1;

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Qy           7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
               :| | | ::: || |  : ||||:|:| : |   |||||:|:||||: :| :     :
Db          20 KRRGAISYDSSDQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSA 79

Qy          67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
               : ::|||||||  :||: ||    : | :|||| |||: || ||| |:||||||||||
Db          80 RNIRRLLSFQRYLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLT 139

Qy         127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
               ||||||:|  |||: |||| :| |||| | |||||:|||||||||||||||||||||||
Db         140 NGNSLVSLTFHLFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 199

Qy         187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
               |||||||||| :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db         200 CYLKEPKLASSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHH 259

Qy         247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
               ||| :|:|||| | :||| |  |::| |:|:|||||||:||||:|:  ::||   || |:
Db         260 WRSAVGLLRESGLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLD 319

Qy         307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
               | : || :||:||||||||||| ||:|||||:| |||: ||::|:|: | :||||::|
Db         320 DGRHRHLVLQMALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQ 379

Qy         367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
                :|| :||||||:|:||||| ||| |:  : ||: ||||:  ||| || | :|  | :
Db         380 TESIANIQIGFMTYLVEPLFTEWARFSA-TRLSQTMLGHVGLNKASWKGLQRQQPSSEDA 438

Qy         427 SGS 429
               : :
Db         439 NAA 441
```

RESULT 11

```
Q6P5G2_MOUSE
ID   Q6P5G2_MOUSE PRELIMINARY;      PRT;   482 AA.
AC   Q6P5G2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Pde7a protein.
GN   Name=Pde7a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062909; AAH62909.1; -; mRNA.
DR   MGI; MGI:1202402; Pde7a.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   482 AA;  55189 MW;  F8460DD84BFE7B65 CRC64;

  Query Match             59.2%;  Score 1424.5;  DB 2;  Length 482;
  Best Local Similarity   62.2%;  Pred. No. 7.3e-102;
  Matches  263;  Conservative   71;  Mismatches   88;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |   |||||:|:||||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||: ||    : | :|||| |||: || ||| |:||||||||||
Db        106 RNIRRLLSFQRYLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||| | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||| :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLASSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  |::| |:|:|||||||:||||:|:  ::||   || |:
Db        286 WRSAVGLLRESGLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLD 345

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              |   || :||:|||||||||||| ||:||||||:| |||: ||::|:|: | :||||::|
Db        346 DGGHRHLVLQMALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQ 405

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
               :|| :||||||:|:|||||| ||| |: :: ||: ||||:  ||| || |  :|  |  :
Db        406 TESIANIQIGFMTYLVEPLFTEWARFS-DTRLSQTMLGHVGLNKASWKGLQRQQPSSEDA 464

Qy        427 SGS 429
              : :
Db        465 NAA 467


RESULT 12
PDE7A_HUMAN
ID   PDE7A_HUMAN    STANDARD;      PRT;   482 AA.
AC   Q13946; O15380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (HCP1) (TM22).
GN   Name=PDE7A;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM PDE7A1).
RX   MEDLINE=93286141; PubMed=8389765;
RA   Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,
RA   Riggs M., Rodgers L., Beavo J.A., Wigler M.;
RT   "Isolation and characterization of a previously undetected human cAMP
RT   phosphodiesterase by complementation of cAMP phosphodiesterase-
RT   deficient Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 268:12925-12932(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM PDE7A2).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97341143; PubMed=9195912; DOI=10.1074/jbc.272.26.16152;
RA   Han P., Zhu X., Michaeli T.;
RT   "Alternative splicing of the high affinity cAMP-specific
RT   phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";
RL   J. Biol. Chem. 272:16152-16157(1997).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SUBCELLULAR LOCATION: PDE7A1 (57 kDa) is located mostly to soluble
CC       cellular fractions. PDE7A2 (50 kDa) is located to particulate
CC       cellular fractions.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=PDE7A1;
CC         IsoId=Q13946-1; Sequence=Displayed;
CC       Name=PDE7A2;
CC         IsoId=Q13946-2; Sequence=VSP_004593;
CC   -!- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal
CC       muscle and at low levels in a variety of tissues including brain
CC       and heart. It is expressed as well in two T-cell lines. PDE7A2 is
CC       found abundantly in skeletal muscle and at low levels in heart.
CC   -!- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2
CC       are found in several fetal tissues, expression is reduced
```

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CC       throughout development. It persists strongly only in adult
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; L12052; AAA35644.2; -; mRNA.
DR   EMBL; U67932; AAB65772.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   HGNC; HGNC:8791; PDE7A.
DR   MIM; 171885; -.
DR   GO; GO:0000267; C:cell fraction; NAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Alternative splicing; cAMP; Hydrolase; Phosphorylation.
FT   REGION      187    451       Catalytic (By similarity).
FT   COMPBIAS     28     33       Poly-Ser.
FT   MOD_RES      84     84       Phosphoserine (Potential).
FT   VARSPLIC      1     46       MEVCYQLPVLPLDRPVPQHVLSRRGAISFSSSSALFGCPNP
FT                                RQLSQ -> MGITLIWCLALVLIKWITSK (in isoform
FT                                PDE7A2).
FT                                /FTId=VSP_004593.
SQ   SEQUENCE   482 AA;  55505 MW;  3B3C8F6E9154F88C CRC64;

  Query Match             58.9%;  Score 1419.5;  DB 1;  Length 482;
  Best Local Similarity   61.7%;  Pred. No. 1.8e-101;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||       |::||:|| |||: || ||| |:||||||||
Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:|||||||:||||:|:  ::||    || ||
Db        286 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 345

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:||||||||||| ||:||||||:| |||: ||::|:|: | :||||::
Db        346 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 405

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:||||| ||| |: |: ||: |||| |||  | |  |  | :
Db        406 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 464

Qy        427 SGS 429
                :
Db        465 DAA 467


RESULT 13
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Q5R5B5_PONPY
ID   Q5R5B5_PONPY PRELIMINARY;      PRT;   456 AA.
AC   Q5R5B5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp469E1731.
GN   Name=DKFZp469E1731;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR860948; CAH93051.1; -; mRNA.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   456 AA;  52755 MW;  CB162B0BFEF074BF CRC64;

  Query Match             58.9%;  Score 1418.5;  DB 2;  Length 456;
  Best Local Similarity   61.7%;  Pred. No. 2e-101;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         20 KRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 79

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||       |::||:|| |||: || ||| |:||||||||
Db         80 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 139

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        140 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 199

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        200 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 259

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:|||||||:||||:|:  ::||    || ||
Db        260 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 319

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:||||||||||| ||:||||||:| |||: ||::|:|: | :||||::
Db        320 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 379

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:||||| ||| |: |: ||: |||| |||  | |  |  | :
Db        380 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 438

Qy        427 SGS 429
                :
Db        439 DAT 441


RESULT 14
PDE7A_RAT
ID   PDE7A_RAT      STANDARD;      PRT;   426 AA.
```

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AC   O08593;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
DE   (Fragment).
GN   Name=Pde7a;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98176136; PubMed=9515162;
RA   Hoffmann R., Abdel'Al S., Engels P.;
RT   "Differential distribution of rat PDE-7 mRNA in embryonic and adult
RT   rat brain.";
RL   Cell Biochem. Biophys. 28:103-113(1998).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction (By similarity).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By
CC       similarity).
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U77880; AAB51234.1; -; mRNA.
DR   HSSP; Q08499; 1MKD.
DR   RGD; 68391; Pde7a.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   cAMP; Hydrolase.
FT   REGION      131    395       Catalytic (By similarity).
FT   NON_TER       1      1
SQ   SEQUENCE   426 AA;  49274 MW;  129BDC01C9351D26 CRC64;

  Query Match             58.0%;  Score 1397.5;  DB 1;  Length 426;
  Best Local Similarity   62.4%;  Pred. No. 7.7e-100;
  Matches  257;  Conservative   68;  Mismatches   86;  Indels    1;  Gaps    1;

Qy         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77
              || |  : ||||:|:|: |  |   |||||:|:||||: :: :      : : ::|||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
              |  :||  ||       |::|||| |||: || ||| |:|||||||||||||||:|  |
Db         61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
              ||: |||| :| |||| | |||||:|||||||||||||||||||||||||||||||||:
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257
              :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||||| :|:||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317
              | :||| |   ::| |:|:|||||||:||||:|:  ::||    || |:| : || :||:
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377
              |||||||||||| ||:|||||:| ||| ||::|:|: | :||||::| :|| :|||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429
              |:|: |||| ||| |: :: ||: ||||:  ||| || |  :|  |  :| :
Db        361 MTYLQEPLFTEWARFS-DTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAA 411


RESULT 15
Q96T72_HUMAN
ID   Q96T72_HUMAN PRELIMINARY;      PRT;   424 AA.
AC   Q96T72;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21265467; PubMed=11371644; DOI=10.1073/pnas.101131098;
RA   Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;
RT   "T cell activation up-regulates cyclic nucleotide phosphodiesterases
RT   8A1 and 7A3.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).
DR   EMBL; AF332652; AAK57640.1; -; mRNA.
DR   HSSP; Q08499; 1OYN.
DR   Ensembl; ENSG00000171408; Homo sapiens.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phos_hydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase_I; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ   SEQUENCE   424 AA;  48827 MW;  A7DBF40D08A7B561 CRC64;

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Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         46 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 105

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||      |::||:|| |||: || ||| |:||||||||||
Db        106 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 165

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        166 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 225

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        226 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 285

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||
Db        286 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 345
```

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Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:||||||||||||| ||:||||||:| ||||: ||::|:|: | :||||::
Db        346 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 405

Qy        367 KDSIPSIQIGFMSYI 381
               :|| :|||| :|:
Db        406 TESIANIQIGNYTYL 420
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Search completed: March 10, 2006, 20:02:08
Job time : 189.805 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 10, 2006, 20:02:25 ; Search time 40.8537 Seconds
(without alignments)
910.666 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2258 | 93.8 | 502 | 2 | US-09-330-970-1 | Sequence 1, Appli |
| 2 | 2051 | 85.2 | 390 | 2 | US-09-949-016-10020 | Sequence 10020, A |
| 3 | 1419.5 | 58.9 | 498 | 1 | US-07-688-352C-20 | Sequence 20, Appl |
| 4 | 1419.5 | 58.9 | 498 | 1 | US-08-474-379C-20 | Sequence 20, Appl |
| 5 | 1419.5 | 58.9 | 498 | 2 | US-09-146-249A-20 | Sequence 20, Appl |
| 6 | 1419.5 | 58.9 | 498 | 2 | US-08-206-188B-20 | Sequence 20, Appl |
| 7 | 1280 | 53.2 | 320 | 2 | US-09-330-970-3 | Sequence 3, Appli |
| 8 | 604.5 | 25.1 | 518 | 2 | US-09-602-735B-2 | Sequence 2, Appli |
| 9 | 604.5 | 25.1 | 673 | 1 | US-08-474-379C-63 | Sequence 63, Appl |
| 10 | 604.5 | 25.1 | 673 | 2 | US-09-146-249A-63 | Sequence 63, Appl |
| 11 | 604.5 | 25.1 | 673 | 2 | US-08-206-188B-63 | Sequence 63, Appl |
| 12 | 603.5 | 25.1 | 517 | 2 | US-09-602-735B-4 | Sequence 4, Appli |
| 13 | 599.5 | 24.9 | 673 | 1 | US-08-577-492-35 | Sequence 35, Appl |
| 14 | 599.5 | 24.9 | 673 | 2 | US-09-079-630-35 | Sequence 35, Appl |
| 15 | 580.5 | 24.1 | 562 | 1 | US-07-688-352C-4 | Sequence 4, Appli |
| 16 | 580.5 | 24.1 | 562 | 1 | US-08-942-521B-8 | Sequence 8, Appli |
| 17 | 580.5 | 24.1 | 562 | 1 | US-08-474-379C-4 | Sequence 4, Appli |
| 18 | 580.5 | 24.1 | 562 | 2 | US-09-146-249A-4 | Sequence 4, Appli |
| 19 | 580.5 | 24.1 | 562 | 2 | US-08-206-188B-4 | Sequence 4, Appli |
| 20 | 580.5 | 24.1 | 562 | 4 | PCT-US91-02714-4 | Sequence 4, Appli |
| 21 | 574.5 | 23.9 | 721 | 2 | US-09-983-754-2 | Sequence 2, Appli |
| 22 | 567.5 | 23.6 | 564 | 1 | US-08-577-492-34 | Sequence 34, Appl |
| 23 | 567.5 | 23.6 | 564 | 1 | US-08-942-521B-2 | Sequence 2, Appli |
| 24 | 567.5 | 23.6 | 564 | 1 | US-08-474-379C-59 | Sequence 59, Appl |
| 25 | 567.5 | 23.6 | 564 | 2 | US-09-146-249A-59 | Sequence 59, Appl |
| 26 | 567.5 | 23.6 | 564 | 2 | US-08-206-188B-59 | Sequence 59, Appl |
| 27 | 567.5 | 23.6 | 564 | 2 | US-09-192-702-2 | Sequence 2, Appli |
| 28 | 567.5 | 23.6 | 564 | 2 | US-09-079-630-34 | Sequence 34, Appl |
| 29 | 567.5 | 23.6 | 564 | 2 | US-08-445-474-2 | Sequence 2, Appli |
| 30 | 567.5 | 23.6 | 564 | 2 | US-09-983-754-4 | Sequence 4, Appli |
| 31 | 567.5 | 23.6 | 564 | 4 | PCT-US94-02612-2 | Sequence 2, Appli |
| 32 | 567.5 | 23.6 | 736 | 1 | US-07-688-352C-24 | Sequence 24, Appl |
| 33 | 567.5 | 23.6 | 736 | 1 | US-08-474-379C-24 | Sequence 24, Appl |
| 34 | 567.5 | 23.6 | 736 | 2 | US-09-146-249A-24 | Sequence 24, Appl |
| 35 | 567.5 | 23.6 | 736 | 2 | US-08-206-188B-24 | Sequence 24, Appl |
| 36 | 567.5 | 23.6 | 736 | 4 | PCT-US91-02714-23 | Sequence 23, Appl |
| 37 | 565 | 23.5 | 885 | 1 | US-08-577-492-33 | Sequence 33, Appl |
| 38 | 565 | 23.5 | 885 | 2 | US-09-079-630-33 | Sequence 33, Appl |
| 39 | 565 | 23.5 | 886 | 1 | US-08-474-379C-65 | Sequence 65, Appl |
| 40 | 565 | 23.5 | 886 | 2 | US-09-146-249A-65 | Sequence 65, Appl |
| 41 | 565 | 23.5 | 886 | 2 | US-08-206-188B-65 | Sequence 65, Appl |
| 42 | 565 | 23.5 | 901 | 2 | US-09-917-254-93 | Sequence 93, Appl |
| 43 | 563 | 23.4 | 686 | 1 | US-08-942-521B-9 | Sequence 9, Appli |
| 44 | 562 | 23.3 | 606 | 1 | US-08-577-492-32 | Sequence 32, Appl |
| 45 | 562 | 23.3 | 606 | 2 | US-09-079-630-32 | Sequence 32, Appl |

ALIGNMENTS

RESULT 1
US-09-330-970-1
; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phophodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-1

Query Match 93.8%; Score 2258; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2e-229;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439
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Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 2
US-09-949-016-10020
; Sequence 10020, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10020
;   LENGTH: 390
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10020

  Query Match             85.2%;  Score 2051;  DB 2;  Length 390;
  Best Local Similarity   92.4%;  Pred. No. 6.1e-208;
  Matches  390;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy         29 DIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGI 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGI 60

Qy         89 IPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHF 148
              ||||||||||||||||||||||||||||||||||||
Db         61 IPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTN---------------------- 99

Qy        149 KLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLL 208
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 -----------VMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLL 148

Qy        209 AAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 208

Qy        269 QDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPC 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 QDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPC 268

Qy        329 RIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFRE 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 RIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFRE 328

Qy        389 WAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEGD 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 WAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEGD 388

Qy        449 SP 450
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Db        389 SP 390


RESULT 3
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US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/688,352C
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-688-352C-20

  Query Match             58.9%;  Score 1419.5;  DB 1;  Length 498;
  Best Local Similarity   61.7%;  Pred. No. 5.2e-141;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : |||:|:| : |  :|||||:|:||||: :| :       :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::|||||||  :||  ||       |::||:|| |||: || ||| |:||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:||||||:||||:|:  ::||   || ||
Db        302 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 361

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:||||||||||| ||:|||||:| ||||: ||::|:|: | :||||::
Db        362 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 421
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Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
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Db        422 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 480

Qy        427 SGS 429
                :
Db        481 DAA 483


RESULT 4
US-08-474-379C-20
; Sequence 20, Application US/08474379C
; Patent No. 5977305
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  CLONING BY COMPLEMENTATION AND RELATED
;    TITLE OF INVENTION:  PROCESSES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,379C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/206,188
;      FILING DATE:  01-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/688,352
;      FILING DATE:  19-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  27866/32771
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-474-379C-20

  Query Match             58.9%;  Score 1419.5;  DB 1;  Length 498;
  Best Local Similarity   61.7%;  Pred. No. 5.2e-141;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::||||||||  :||  ||       |::||:|| |||: || ||| |:||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
              ||||||:|  |||: |||| :| |||: | |||||:|||||||||||||||||||||||
Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||
Db        302 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 361

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
              | : || :||:|||||||||||| ||:|||||:| ||||: ||::|:|: | :||||::
Db        362 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 421

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:|||||| ||| |: |: ||: ||||:  ||| || |   | | :
Db        422 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 480

Qy        427 SGS 429
                :
Db        481 DAA 483


RESULT 5
US-09-146-249A-20
; Sequence 20, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-20

  Query Match             58.9%;  Score 1419.5;  DB 2;  Length 498;
  Best Local Similarity   61.7%;  Pred. No. 5.2e-141;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;
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Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::||||||||  :||  ||      |::||:|| ||||: || ||| |:||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
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Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
              ||| :|:|||| | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||
Db        302 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 361

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
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Db        362 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 421

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:||||| ||| |: |: ||: ||||:  ||| || |   | |  :
Db        422 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 480

Qy        427 SGS 429
                :
Db        481 DAA 483


RESULT 6
US-08-206-188B-20
; Sequence 20, Application US/08206188B
; Patent No. 6100025
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/206,188B
;      FILING DATE:  01-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-206-188B-20

  Query Match             58.9%;  Score 1419.5;  DB 2;  Length 498;
  Best Local Similarity   61.7%;  Pred. No. 5.2e-141;
  Matches  261;  Conservative   70;  Mismatches   91;  Indels    1;  Gaps    1;

Qy          7 ERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTK 66
              :| | | ::: || |  : ||||:|:| : |  :|||||:|:||||: :| :      :
Db         62 QRRGAISYDSSDQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSA 121

Qy         67 KKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLT 126
              : ::||||||||  :||  ||      |::||:|| ||||: || ||| |:||||||||
Db        122 RNIRRLLSFQRYLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLT 181

Qy        127 NGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMH 186
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Db        182 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 241

Qy        187 CYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHH 246
              |||||||||: :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||
Db        242 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 301

Qy        247 WRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLE 306
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Db        302 WRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLE 361

Qy        307 DAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQ 366
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Db        362 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 421

Qy        367 KDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGS 426
              :|| :||||||:|:||||| ||| |: |: ||: ||||:  ||| || |   | |  :
Db        422 TESIANIQIGFMTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDT 480

Qy        427 SGS 429
                :
Db        481 DAA 483


RESULT 7
US-09-330-970-3
; Sequence 3, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT: White, David
;  TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
;  TITLE OF INVENTION: Phophodiesterase
;  FILE REFERENCE: 5800-28
;  CURRENT APPLICATION NUMBER: US/09/330,970
;  CURRENT FILING DATE: 1999-06-11
;  EARLIER APPLICATION NUMBER: 09/277,423
;  EARLIER FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 320
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-330-970-3

  Query Match             53.2%;  Score 1280;  DB 2;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-126;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139
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Qy          88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy         148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy         208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy         268 T 268
               |
Db         320 T 320


RESULT 8
US-09-602-735B-2
; Sequence 2, Application US/09602735B
; Patent No. 6656717
; GENERAL INFORMATION:
;  APPLICANT: Xin, Xiaonan
;  APPLICANT:  Unterbeck, Axel
;  APPLICANT:  Hu, Yinghe
;  TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 453260-55
;  CURRENT APPLICATION NUMBER: US/09/602,735B
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: U.S. 60/141,196
;  PRIOR FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 518
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-602-735B-2

  Query Match             25.1%;  Score 604.5;  DB 2;  Length 518;
  Best Local Similarity   33.3%;  Pred. No. 8e-55;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|      ::  |:| |    ||:  :    || | :    | | |   :|
Db          63 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 119

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
               | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         120 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 178

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         179 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 238

Qy         241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
               ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         239 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 298

Qy         299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
               |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db         299 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 358

Qy         353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
               ::  :||||:|::   |:  |:||: ||| ||:  ||         ::::|  |  |:
Db         359 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 416

Qy         413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
               ::| :|:      |    ||    |:  ::|        |::|:|
Db         417 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 455
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RESULT 9
US-08-474-379C-63
; Sequence 63, Application US/08474379C
; Patent No. 5977305
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  CLONING BY COMPLEMENTATION AND RELATED
;    TITLE OF INVENTION:  PROCESSES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,379C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/206,188
;      FILING DATE:  01-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/688,352
;      FILING DATE:  19-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  27866/32771
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-474-379C-63

  Query Match             25.1%;  Score 604.5;  DB 1;  Length 673;
  Best Local Similarity   33.3%;  Pred. No. 1.2e-54;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|      ::  |:| |    ||:  :    || | :    | | |   :|
Db         218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE--,-LEDVNKWGLHVFR 274

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
               | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy         241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
               ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy         299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
               |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db         454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513
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Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  | |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|       |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 610


RESULT 10
US-09-146-249A-63
; Sequence 63, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-63

  Query Match           25.1%;  Score 604.5;  DB 2;  Length 673;
  Best Local Similarity   33.3%;  Pred. No. 1.2e-54;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | |  : |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|   :  :| |:  | : : :  ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453
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Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
              |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  | |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|       |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 610


RESULT 11
US-08-206-188B-63
; Sequence 63, Application US/08206188B
; Patent No. 6100025
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/206,188B
;      FILING DATE:  01-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-206-188B-63

  Query Match           25.1%;  Score 604.5;  DB 2;  Length 673;
  Best Local Similarity   33.3%;  Pred. No. 1.2e-54;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | |  : |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393
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Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |      | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||     |:  ::|         |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 610


RESULT 12
US-09-602-735B-4
; Sequence 4, Application US/09602735B
; Patent No. 6656717
; GENERAL INFORMATION:
;  APPLICANT: Xin, Xiaonan
;  APPLICANT:  Unterbeck, Axel
;  APPLICANT:  Hu, Yinghe
;  TITLE OF INVENTION: Cyclic AMP Phosphodiesterase Isoforms and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 453260-55
;  CURRENT APPLICATION NUMBER: US/09/602,735B
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: U.S. 60/141,196
;  PRIOR FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 517
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-602-735B-4

  Query Match           25.1%;  Score 603.5;  DB 2;  Length 517;
  Best Local Similarity   33.3%;  Pred. No. 1e-54;
  Matches  135;  Conservative   85;  Mismatches  152;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|      ::  |:| |    ||:  :    || | :    |  |  |   :|
Db         63 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 119

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        120 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 178

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | |  :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        179 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 238

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :    ::||||:::    |  ||  :
Db        239 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMV 298

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |      | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        299 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 358

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        359 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 416

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||     |:  ::|         |::|:|
Db        417 YQSTIPQ------SPSPAPDDQEDGRQGQTEKFQFELTLEEDGES 455


RESULT 13
US-08-577-492-35
; Sequence 35, Application US/08577492
; Patent No. 5851784
;  GENERAL INFORMATION:
;    APPLICANT:  Owens, Raymond John
;    APPLICANT:  Perry, Martin John
;    APPLICANT:  Lumb, Simon Mark
;    TITLE OF INVENTION:  HUMAN PHOSPHODIESTERASE TYPE IVC, AND
;    TITLE OF INVENTION:  ITS PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/577,492
;      FILING DATE:  22-DEC-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9426227.6
;      FILING DATE:  23-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9512996.1
;      FILING DATE:  26-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherry, David A.
;      REGISTRATION NUMBER:  35,099
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
US-08-577-492-35

  Query Match           24.9%;  Score 599.5;  DB 1;  Length 673;
  Best Local Similarity   33.6%;  Pred. No. 4.1e-54;
  Matches  136;  Conservative   84;  Mismatches  152;  Indels   33;  Gaps   10;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|      ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | |  :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :    ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |      | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
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Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAG-QGTESE-------EQEGDS 449
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Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTGKFQFELTLEEDGES 610


RESULT 14
US-09-079-630-35
; Sequence 35, Application US/09079630
; Patent No. 6291199
;  GENERAL INFORMATION:
;    APPLICANT:  Owens, Raymond John
;    APPLICANT:  Perry, Martin John
;    APPLICANT:  Lumb, Simon Mark
;    TITLE OF INVENTION:  HUMAN PHOSPHODIESTERASE TYPE IVC, AND
;    TITLE OF INVENTION:  ITS PRODUCTION AND USE
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,630
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/577,492
;      FILING DATE:  22-DEC-1995
;      APPLICATION NUMBER:  GB 9426227.6
;      FILING DATE:  23-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9512996.1
;      FILING DATE:  26-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherry, David A.
;      REGISTRATION NUMBER:  35,099
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  673 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
US-09-079-630-35

  Query Match             24.9%;  Score 599.5;  DB 2;  Length 673;
  Best Local Similarity   33.6%;  Pred. No. 4.1e-54;
  Matches  136;  Conservative   84;  Mismatches  152;  Indels   33;  Gaps   10;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|     |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| |||||||||:  ||| ||  || :| : |
Db        334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAG-QGTESE-------EQEGDS 449
              ::| :|:     |    ||     | ||   :       |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTGKFQFELTLEEDGES 610


RESULT 15
US-07-688-352C-4
; Sequence 4, Application US/07688352C
; Patent No. 5527896
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/688,352C
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-688-352C-4

  Query Match             24.1%;  Score 580.5;  DB 1;  Length 562;
  Best Local Similarity   31.9%;  Pred. No. 3.1e-52;
  Matches  130;  Conservative   91;  Mismatches  159;  Indels   27;  Gaps    7;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              ||| ::|::     ::  |:| |    | :  ::  :||:| :    |:|   |  :||
Db        124 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 180

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                 ::   |  ::  :|    |:  ||:   |  ::: ::: |||   |||::|||||
Db        181 VAGYSHNRPLTCIMYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADV 240
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Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
Db        241 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 300

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
Db        301 LENHHLAVGFKLLQEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 360

Qy        300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
Db        361 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 420

Qy        354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
Db        421 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 478

Qy        414 KSLLPR------QHRSRGSSGSGPDHDH----AGQGTESEEQEGDSP 450
Db        479 QSMIPQSPSPPLDERSRDCQGLMEKFQFELTLEEEDSEGPEKEGEGP 525
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Search completed: March 10, 2006, 20:04:14
Job time : 41.8537 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:18:07 ; Search time 135.976 Seconds
(without alignments)
1382.771 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2408 | 100.0 | 450 | 4 | US-10-781-181-5 | Sequence 5, Appli |
| 2 | 2408 | 100.0 | 450 | 5 | US-10-204-268A-2 | Sequence 2, Appli |
| 3 | 2258 | 93.8 | 502 | 4 | US-10-273-517-1 | Sequence 1, Appli |
| 4 | 2258 | 93.8 | 502 | 4 | US-10-386-414-4 | Sequence 4, Appli |
| 5 | 2258 | 93.8 | 502 | 4 | US-10-311-104-1 | Sequence 1, Appli |
| 6 | 2258 | 93.8 | 502 | 6 | US-11-048-744-1 | Sequence 1, Appli |
| 7 | 2258 | 93.8 | 502 | 6 | US-11-048-068-1 | Sequence 1, Appli |
| 8 | 2192 | 91.0 | 446 | 4 | US-10-781-181-1 | Sequence 1, Appli |
| 9 | 1865 | 77.5 | 391 | 5 | US-10-204-268A-4 | Sequence 4, Appli |
| 10 | 1801 | 74.8 | 335 | 5 | US-10-771-833-23 | Sequence 23, Appl |
| 11 | 1801 | 74.8 | 335 | 5 | US-10-886-949-23 | Sequence 23, Appl |
| 12 | 1430 | 59.4 | 288 | 4 | US-10-781-181-3 | Sequence 3, Appli |
| 13 | 1410.5 | 58.6 | 426 | 3 | US-09-966-781A-2 | Sequence 2, Appli |
| 14 | 1403.5 | 58.3 | 426 | 3 | US-09-966-781A-1 | Sequence 1, Appli |
| 15 | 1397.5 | 58.0 | 426 | 3 | US-09-966-781A-3 | Sequence 3, Appli |
| 16 | 1287 | 53.4 | 424 | 5 | US-10-380-437-6 | Sequence 6, Appli |
| 17 | 1287 | 53.4 | 424 | 5 | US-10-380-437-53 | Sequence 53, Appl |
| 18 | 1286 | 53.4 | 432 | 3 | US-09-764-898-208 | Sequence 208, App |
| 19 | 1280 | 53.2 | 320 | 4 | US-10-386-414-6 | Sequence 6, Appli |
| 20 | 1234.5 | 51.3 | 334 | 5 | US-10-771-833-22 | Sequence 22, Appl |
| 21 | 1234.5 | 51.3 | 334 | 5 | US-10-886-949-22 | Sequence 22, Appl |
| 22 | 1194.5 | 49.6 | 336 | 4 | US-10-258-746-2 | Sequence 2, Appli |
| 23 | 771 | 32.0 | 211 | 3 | US-09-764-898-280 | Sequence 280, App |
| 24 | 771 | 32.0 | 211 | 3 | US-09-989-442-120 | Sequence 120, App |
| 25 | 604.5 | 25.1 | 507 | 4 | US-10-076-597-49 | Sequence 49, Appl |
| 26 | 604.5 | 25.1 | 507 | 4 | US-10-067-514-10 | Sequence 10, Appl |
| 27 | 604.5 | 25.1 | 507 | 4 | US-10-419-723-10 | Sequence 10, Appl |
| 28 | 604.5 | 25.1 | 507 | 4 | US-10-255-120-10 | Sequence 10, Appl |
| 29 | 604.5 | 25.1 | 507 | 4 | US-10-755-889-304 | Sequence 304, App |
| 30 | 604.5 | 25.1 | 507 | 5 | US-10-868-397-10 | Sequence 10, Appl |
| 31 | 604.5 | 25.1 | 518 | 4 | US-10-682-722-2 | Sequence 2, Appli |
| 32 | 604.5 | 25.1 | 585 | 4 | US-10-067-514-9 | Sequence 9, Appli |
| 33 | 604.5 | 25.1 | 585 | 4 | US-10-419-723-9 | Sequence 9, Appli |
| 34 | 604.5 | 25.1 | 585 | 4 | US-10-255-120-9 | Sequence 9, Appli |
| 35 | 604.5 | 25.1 | 585 | 5 | US-10-868-397-9 | Sequence 9, Appli |
| 36 | 604.5 | 25.1 | 664 | 5 | US-10-735-973-2 | Sequence 2, Appli |
| 37 | 604.5 | 25.1 | 673 | 4 | US-10-076-597-51 | Sequence 51, Appl |
| 38 | 604.5 | 25.1 | 673 | 4 | US-10-067-514-6 | Sequence 6, Appli |
| 39 | 604.5 | 25.1 | 673 | 4 | US-10-419-723-6 | Sequence 6, Appli |
| 40 | 604.5 | 25.1 | 673 | 4 | US-10-255-120-6 | Sequence 6, Appli |
| 41 | 604.5 | 25.1 | 673 | 4 | US-10-239-439-4 | Sequence 4, Appli |
| 42 | 604.5 | 25.1 | 673 | 5 | US-10-684-206-36 | Sequence 36, Appl |
| 43 | 604.5 | 25.1 | 673 | 5 | US-10-735-973-1 | Sequence 1, Appli |
| 44 | 604.5 | 25.1 | 679 | 5 | US-10-735-973-6 | Sequence 6, Appli |
| 45 | 604.5 | 25.1 | 687 | 4 | US-10-067-514-8 | Sequence 8, Appli |

ALIGNMENTS

RESULT 1
US-10-781-181-5
; Sequence 5, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: Enzyme PDE xiv
; FILE REFERENCE: PC10315B
; CURRENT APPLICATION NUMBER: US/10/781,181
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: GB 9828603.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/471,459
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 9922123.6
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Human
US-10-781-181-5

Query Match 100.0%; Score 2408; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 9.2e-226;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
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Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
                |||||||||||||||||||||||||||||
Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 2
US-10-204-268A-2
; Sequence 2, Application US/10204268A
; Publication No. US20050058647A1
; GENERAL INFORMATION:
;  APPLICANT: KLUXEN, FRANZ-WERNER
;  APPLICANT:  HENTSCH, BERND
;  TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
;  FILE REFERENCE: MERCK-2484
;  CURRENT APPLICATION NUMBER: US/10/204,268A
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: PCT/EP01/01858
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: EP 00103655.7
;  PRIOR FILING DATE: 2000-02-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-204-268A-2

  Query Match           100.0%;  Score 2408;  DB 5;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-226;
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450
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Db        421 HRSRGSSGSGPDHDHAGQGTESEEQEGDSP 450


RESULT 3
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US-10-273-517-1
; Sequence 1, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:
;  APPLICANT: THORNTON, Michael B.; DING, Li
;  APPLICANT:  ARVIZU, Chandra S.; YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.; LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.; BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; LU, Yan
;  APPLICANT:  CHAWLA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 USA
;  CURRENT APPLICATION NUMBER: US/10/273,517
;  CURRENT FILING DATE:  2002-10-18
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1
US-10-273-517-1

  Query Match           93.8%;  Score 2258;  DB 4;  Length 502;
  Best Local Similarity  100.0%;  Pred. No. 4.7e-211;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 4
US-10-386-414-4
; Sequence 4, Application US/10386414
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; Publication No. US20040006016A1
; GENERAL INFORMATION:
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT:  Robison, Keith E.
;  APPLICANT:  White, David
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Cook, William James
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
;  TITLE OF INVENTION:  55092 AND 10218 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-021OMNIM
;  CURRENT APPLICATION NUMBER: US/10/386,414
;  CURRENT FILING DATE:  2003-03-11
;  PRIOR APPLICATION NUMBER: 09/426,282
;  PRIOR FILING DATE: 1999-10-25
;  PRIOR APPLICATION NUMBER: 09/668,266
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/330,970
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: 09/724,599
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/860,193
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: 10/283,023
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,044
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/010,943
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 60/254,037
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: 09/833,082
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-386-414-4

  Query Match             93.8%;  Score 2258;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-211;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 5
US-10-311-104-1
; Sequence 1, Application US/10311104
; Publication No. US20040054138A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  DING, Li
;  APPLICANT:  ARIVZU Chandra S.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  LU, Yan
;  APPLICANT:  Chawla, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,104
;  CURRENT FILING DATE:  2002-12-12
;  PRIOR APPLICATION NUMBER: PCT/US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
US-10-311-104-1

  Query Match             93.8%;  Score 2258;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-211;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 6
US-11-048-744-1
; Sequence 1, Application US/11048744
; Publication No. US20050164275A1
; GENERAL INFORMATION:
;  APPLICANT: THORNTON, Michael B.; DING, Li
;  APPLICANT:  ARVIZU, Chandra S.; YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.; LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.; BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi; LU, Yan
;  APPLICANT:  CHAWLA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 USA
;  CURRENT APPLICATION NUMBER: US/11/048,744
;  CURRENT FILING DATE:  2005-02-03
;  PRIOR APPLICATION NUMBER: US/10/273,517
;  PRIOR FILING DATE: 2002-10-18
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7476201CD1
US-11-048-744-1

  Query Match             93.8%;  Score 2258;  DB 6;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-211;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
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Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 7
US-11-048-068-1
; Sequence 1, Application US/11048068
; Publication No. US20050202478A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  DING, Li
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  HAFALIA, April J. A.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  LU, Yan
;  APPLICANT:  WALIA, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 PCT
;  CURRENT APPLICATION NUMBER: US/11/048,068
;  CURRENT FILING DATE:  2005-02-02
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7476201CD1
US-11-048-068-1

  Query Match             93.8%;  Score 2258;  DB 6;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-211;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
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Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
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Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439
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Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
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Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
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Db        500 DSP 502


RESULT 8
US-10-781-181-1
; Sequence 1, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Enzyme PDE xiv
;  FILE REFERENCE: PC10315B
;  CURRENT APPLICATION NUMBER: US/10/781,181
;  CURRENT FILING DATE:  2004-02-18
;  PRIOR APPLICATION NUMBER: GB 9828603.2
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: US 09/471,459
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: GB 9922123.6
;  PRIOR FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Mouse
US-10-781-181-1

  Query Match             91.0%;  Score 2192;  DB 4;  Length 446;
  Best Local Similarity   91.6%;  Pred. No. 1.1e-204;
  Matches  413;  Conservative   13;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
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Db          1 MSCLMVERCGEVLFESPEQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              |||||||||||||||||:|||||||||||||||||||||||||  ||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN 300

Qy        301 KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS 360
              ||||||: ||||||||||||||||||||||||||||||||||||||:||||||||||
Db        301 KDLRLENVQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS 360

Qy        361 PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ 420
              ||||||||||||||||:|||||||||| |||||||||||| ||||||||||||  |
Db        361 PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420

Qy        421 HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP 450
              || |||       | ||   |: || || :|
Db        421 HRRRGSG-----QDLAGPAPETLEQTEGATP 446


RESULT 9
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US-10-204-268A-4
; Sequence 4, Application US/10204268A
; Publication No. US20050058647A1
; GENERAL INFORMATION:
;  APPLICANT: KLUXEN, FRANZ-WERNER
;  APPLICANT:  HENTSCH, BERND
;  TITLE OF INVENTION: NEW PHOSPHODIESTERASE TYPE 7B
;  FILE REFERENCE: MERCK-2484
;  CURRENT APPLICATION NUMBER: US/10/204,268A
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: PCT/EP01/01858
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: EP 00103655.7
;  PRIOR FILING DATE: 2000-02-21
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (188)
;   OTHER INFORMATION: Pro or His
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (387)
;   OTHER INFORMATION: Val, Ala, Asp, Glu or Gly
US-10-204-268A-4

  Query Match             77.5%;  Score 1865;  DB 5;  Length 391;
  Best Local Similarity   92.7%;  Pred. No. 7.4e-173;
  Matches  354;  Conservative    2;  Mismatches   26;  Indels    0;  Gaps    0;

Qy         52 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 RLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSK 69

Qy        112 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 VGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNP 129

Qy        172 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHH 231
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        130 YHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNXH 189

Qy        232 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 LANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFL 249

Qy        292 TRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGEL 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGEL 309

Qy        352 EQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKA 411
              |||| |||||||||||||||||||||||     |||||||     ||||
Db        310 EQKFGLEISPLCNQQKDSIPSIQIGFMSYIVEPALPGMAHFTGNSTLQRTCWATFAHNKG 369

Qy        412 QWKSLLPRQHRSRGSSGSGPDH 433
              |||||||    :  :   | ||
Db        370 QWKSLLPSSTEAGAALAXGLDH 391


RESULT 10
US-10-771-833-23
; Sequence 23, Application US/10771833
; Publication No. US20050048573A1
; GENERAL INFORMATION:
;  APPLICANT: MILBURN, MICHAEL V.
;  TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
;  FILE REFERENCE: 039363-1106
;  CURRENT APPLICATION NUMBER: US/10/771,833
;  CURRENT FILING DATE:  2004-02-03
```

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;  PRIOR APPLICATION NUMBER: 60/485,627
;  PRIOR FILING DATE: 2003-07-07
;  PRIOR APPLICATION NUMBER: 60/444,734
;  PRIOR FILING DATE: 2003-02-03
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-771-833-23

  Query Match            74.8%;  Score 1801;  DB 5;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 1e-166;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 60

Qy        147 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 120

Qy        207 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 180

Qy        267 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 240

Qy        327 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 300

Qy        387 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 421
              |||||||||||||||||||||||||||||||||||
Db        301 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 335


RESULT 11
US-10-886-949-23
; Sequence 23, Application US/10886949
; Publication No. US20050079548A1
; GENERAL INFORMATION:
;  APPLICANT: DEAN R. ARTIS
;  APPLICANT:  BOLLAG, GIDEON
;  APPLICANT:  CARD, GRAHAM
;  APPLICANT:  MARTIN, FERNANDO
;  APPLICANT:  MILBURN, MICHAEL V.
;  APPLICANT:  ZHANG, KAM
;  TITLE OF INVENTION: PDE5A CRYSTAL STRUCTURE AND USES
;  FILE REFERENCE: 039363-1108
;  CURRENT APPLICATION NUMBER: US/10/886,949
;  CURRENT FILING DATE:  2004-07-07
;  PRIOR APPLICATION NUMBER: 60/485,627
;  PRIOR FILING DATE: 2003-07-07
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-886-949-23

  Query Match            74.8%;  Score 1801;  DB 5;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 1e-166;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         87 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIH 60

Qy        147 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLG 120

Qy        207 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 180

Qy        267 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICN 240

Qy        327 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLF 300

Qy        387 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 421
              |||||||||||||||||||||||||||||||||||
Db        301 REWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQH 335


RESULT 12
US-10-781-181-3
; Sequence 3, Application US/10781181
; Publication No. US20040137508A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Fidock, Mark David
;  TITLE OF INVENTION: Enzyme PDE xiv
;  FILE REFERENCE: PC10315B
;  CURRENT APPLICATION NUMBER: US/10/781,181
;  CURRENT FILING DATE:  2004-02-18
;  PRIOR APPLICATION NUMBER: GB 9828603.2
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: US 09/471,459
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: GB 9922123.6
;  PRIOR FILING DATE: 1999-09-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Human
US-10-781-181-3

  Query Match            59.4%;  Score 1430;  DB 4;  Length 288;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-130;
  Matches  268;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSCLMVERCGEILFENPDQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS 60

Qy         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GEIGTKKKVKRLLSFQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF 120

Qy        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240

Qy        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268
              ||||||||||||||||||||||||||||
Db        241 VLENHHWRSTIGMLRESRLLAHLPKEMT 268


RESULT 13
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```
US-09-966-781A-2
; Sequence 2, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
;  APPLICANT: SOULARD, PATRICIA
;  TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
;  TITLE OF INVENTION:  SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
;  FILE REFERENCE: A0000281US
;  CURRENT APPLICATION NUMBER: US/09/966,781A
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: EP004026837
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-966-781A-2

  Query Match           58.6%;  Score 1410.5;  DB 3;  Length 426;
  Best Local Similarity   63.1%;  Pred. No. 1.9e-128;
  Matches  260;  Conservative   67;  Mismatches   84;  Indels    1;  Gaps    1;

Qy         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77
              || |  : ||||:|:| : |   |||||:|:||||: :| :       : : ::|||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 60

Qy         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
              |  :||: ||    : | :||||| |||: || ||| |:||||||||||||||||:|  |
Db         61 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
              ||: |||| :| |||| | |||||:|||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 180

Qy        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257
              :|| ||:| |:||| ||:||||||||||||||||:|| ||:| ||||||||| :|:||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 240

Qy        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317
              | :||| |  |::| |:|:|||||||:||||:|:  ::||   || |:| : || :||:
Db        241 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377
              |||||||||||| ||:|||||:| ||| |::|:|:  | :||||::| :|| :|||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429
              |:|:|||| ||| |: : ||: ||||:  ||| || |  :|  |  :: :
Db        361 MTYLVEPLFTEWARFSA-TRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAA 411


RESULT 14
US-09-966-781A-1
; Sequence 1, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
;  APPLICANT: SOULARD, PATRICIA
;  TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
;  TITLE OF INVENTION:  SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
;  FILE REFERENCE: A0000281US
;  CURRENT APPLICATION NUMBER: US/09/966,781A
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: EP004026837
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-966-781A-1

  Query Match           58.3%;  Score 1403.5;  DB 3;  Length 426;
  Best Local Similarity   62.6%;  Pred. No. 9.1e-128;
  Matches  258;  Conservative   66;  Mismatches   87;  Indels    1;  Gaps    1;

Qy         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77
              || |  : ||||:|:| : |   |||||:|:||||: :| :       : : ::|||||||
Db          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60

Qy         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
              |  :||  ||       |::||:|| |||: || ||| |:||||||||||||||||:|  |
Db         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
              ||: |||| :| |||| | |||||:|||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 180

Qy        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257
              :|| ||:| |:||| ||:||||||||||||||||:|| ||:| ||||||||| :|:||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317
              | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:
Db        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

Qy        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377
              |||||||||||| ||:|||||:| ||| |::|:|:  | :||||::  :|| :|||||
Db        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360

Qy        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429
              |:|:|||| ||| |: : ||: ||||:  ||| || |  :|  |  :: :
Db        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411


RESULT 15
US-09-966-781A-3
; Sequence 3, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
;  APPLICANT: SOULARD, PATRICIA
;  TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
;  TITLE OF INVENTION:  SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
;  FILE REFERENCE: A0000281US
;  CURRENT APPLICATION NUMBER: US/09/966,781A
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: EP004026837
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-966-781A-3

  Query Match           58.0%;  Score 1397.5;  DB 3;  Length 426;
  Best Local Similarity   62.4%;  Pred. No. 3.5e-127;
  Matches  257;  Conservative   68;  Mismatches   86;  Indels    1;  Gaps    1;

Qy         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77
              || |  : ||||:|:| : |   |||||:|:||||: :: :       : : ::|||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
              |  :||  ||       |::||||| |||: || ||| |:||||||||||||||||:|  |
Db         61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
              ||: |||| :| |||| | |||||:|||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257
              :|| ||:| |:||| ||:||||||||||||||||:|| ||:| ||||||||| :|:||||
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Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317
              | :||| |   ::| |:|:|||||||:||||:|:  ::||   || |:| : || :||:
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377
              |||||||||||| ||:|||||||:| |||: ||::|:|: | :||||::| :|| :|||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429
              |:|: |||| ||| |: :: ||: |||:  ||| || |  :|  |  :| :
Db        361 MTYLQEPLFTEWARFS-DTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAA 411
```

Search completed: March 10, 2006, 20:22:34
Job time : 136.976 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2006, 20:19:01 ; Search time 17.6829 Seconds
(without alignments)
708.350 Million cell updates/sec

Title: US-10-781-181-5
Perfect score: 2408
Sequence: 1 MSCLMVERCGEILFENPDQN.....PDHDHAGQGTESEEQEGDSP 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2258 | 93.8 | 502 | 7 | US-11-226-701-4 | Sequence 4, Appli |
| 2 | 1280 | 53.2 | 320 | 7 | US-11-226-701-6 | Sequence 6, Appli |
| 3 | 604.5 | 25.1 | 507 | 7 | US-11-091-018-10 | Sequence 10, Appl |
| 4 | 604.5 | 25.1 | 585 | 7 | US-11-091-018-9 | Sequence 9, Appli |
| 5 | 604.5 | 25.1 | 673 | 7 | US-11-091-018-6 | Sequence 6, Appli |
| 6 | 604.5 | 25.1 | 687 | 7 | US-11-091-018-8 | Sequence 8, Appli |
| 7 | 604.5 | 25.1 | 745 | 7 | US-11-091-018-4 | Sequence 4, Appli |
| 8 | 604.5 | 25.1 | 748 | 6 | US-10-492-835-12 | Sequence 12, Appl |
| 9 | 604.5 | 25.1 | 748 | 6 | US-10-492-835-28 | Sequence 28, Appl |
| 10 | 604.5 | 25.1 | 809 | 7 | US-11-091-018-2 | Sequence 2, Appli |
| 11 | 603.5 | 25.1 | 747 | 6 | US-10-492-835-8 | Sequence 8, Appli |
| 12 | 603.5 | 25.1 | 747 | 6 | US-10-492-835-27 | Sequence 27, Appl |
| 13 | 594.5 | 24.7 | 747 | 6 | US-10-492-835-15 | Sequence 15, Appl |
| 14 | 570.5 | 23.7 | 349 | 7 | US-11-123-893-13 | Sequence 13, Appl |
| 15 | 567.5 | 23.6 | 736 | 7 | US-11-169-041-207 | Sequence 207, App |
| 16 | 556.5 | 23.1 | 398 | 7 | US-11-123-893-11 | Sequence 11, Appl |
| 17 | 546.5 | 22.7 | 357 | 7 | US-11-123-893-12 | Sequence 12, Appl |
| 18 | 448.5 | 18.6 | 769 | 7 | US-11-072-512-2646 | Sequence 2646, Ap |
| 19 | 298 | 12.4 | 941 | 6 | US-10-501-035-343 | Sequence 343, App |
| 20 | 277.5 | 11.5 | 854 | 6 | US-10-511-657-4 | Sequence 4, Appli |
| 21 | 191 | 7.9 | 786 | 7 | US-11-072-512-2944 | Sequence 2944, Ap |
| 22 | 103 | 4.3 | 968 | 6 | US-10-501-035-219 | Sequence 219, App |
| 23 | 94.5 | 3.9 | 611 | 7 | US-11-087-099-8358 | Sequence 8358, Ap |
| 24 | 91.5 | 3.8 | 635 | 7 | US-11-096-568A-29628 | Sequence 29628, A |
| 25 | 91.5 | 3.8 | 710 | 7 | US-11-096-568A-29627 | Sequence 29627, A |
| 26 | 90 | 3.7 | 1049 | 7 | US-11-137-465-42 | Sequence 42, Appl |
| 27 | 86 | 3.6 | 418 | 7 | US-11-109-156-2 | Sequence 2, Appli |
| 28 | 83.5 | 3.5 | 937 | 7 | US-11-096-568A-31319 | Sequence 31319, A |
| 29 | 82.5 | 3.4 | 422 | 7 | US-11-230-251-26 | Sequence 26, Appl |
| 30 | 82 | 3.4 | 366 | 7 | US-11-096-568A-5564 | Sequence 5564, Ap |
| 31 | 82 | 3.4 | 372 | 7 | US-11-096-568A-5563 | Sequence 5563, Ap |
| 32 | 82 | 3.4 | 643 | 7 | US-11-096-568A-27797 | Sequence 27797, A |
| 33 | 82 | 3.4 | 1024 | 6 | US-10-131-826A-198 | Sequence 198, App |
| 34 | 82 | 3.4 | 1024 | 6 | US-10-973-115B-198 | Sequence 198, App |
| 35 | 81.5 | 3.4 | 808 | 7 | US-11-072-512-2324 | Sequence 2324, Ap |
| 36 | 81 | 3.4 | 286 | 7 | US-11-072-512-3361 | Sequence 3361, Ap |
| 37 | 81 | 3.4 | 418 | 7 | US-11-099-691-1 | Sequence 1, Appli |
| 38 | 81 | 3.4 | 484 | 7 | US-11-072-512-3381 | Sequence 3381, Ap |
| 39 | 81 | 3.4 | 678 | 7 | US-11-072-512-3832 | Sequence 3832, Ap |
| 40 | 81 | 3.4 | 852 | 6 | US-10-467-657-5004 | Sequence 5004, Ap |
| 41 | 81 | 3.4 | 926 | 7 | US-11-232-405A-34 | Sequence 34, Appl |
| 42 | 81 | 3.4 | 6738 | 6 | US-10-922-232B-56 | Sequence 56, Appl |
| 43 | 80.5 | 3.3 | 326 | 7 | US-11-087-099-1590 | Sequence 1590, Ap |
| 44 | 80.5 | 3.3 | 376 | 7 | US-11-098-686-10379 | Sequence 10379, A |
| 45 | 80.5 | 3.3 | 3487 | 7 | US-11-087-099-10423 | Sequence 10423, A |

ALIGNMENTS

RESULT 1
US-11-226-701-4
; Sequence 4, Application US/11226701
; Publication No. US20060009632A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-021OMNIM
; CURRENT APPLICATION NUMBER: US/11/226,701
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: US/10/386,414
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-226-701-4

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  Query Match             93.8%;  Score 2258;  DB 7;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-201;
  Matches  423;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        328 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        388 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEEQEG 499

Qy        448 DSP 450
              |||
Db        500 DSP 502
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RESULT 2
US-11-226-701-6
; Sequence 6, Application US/11226701
; Publication No. US20060009632A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Kapeller-Libermann, Rosana
;  APPLICANT:  Robison, Keith E.
;  APPLICANT:  White, David
;  APPLICANT:  Williamson, Mark W.
;  APPLICANT:  Cook, William James
;  APPLICANT:  Meyers, Rachel E.
;  APPLICANT:  MacBeth, Kyle J.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Chun, Miyoung
;  TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
;  TITLE OF INVENTION:  55092 AND 10218 MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MPI03-021OMNIM
;  CURRENT APPLICATION NUMBER: US/11/226,701
;  CURRENT FILING DATE:  2005-09-14
;  PRIOR APPLICATION NUMBER: US/10/386,414
;  PRIOR FILING DATE: 2003-03-11
;  PRIOR APPLICATION NUMBER: 09/426,282
;  PRIOR FILING DATE: 1999-10-25
;  PRIOR APPLICATION NUMBER: 09/668,266
;  PRIOR FILING DATE: 2000-09-22
;  PRIOR APPLICATION NUMBER: 09/330,970
;  PRIOR FILING DATE: 1999-06-11
;  PRIOR APPLICATION NUMBER: 09/724,599
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/860,193
;  PRIOR FILING DATE: 2001-05-16
;  PRIOR APPLICATION NUMBER: 09/571,689
;  PRIOR FILING DATE: 2000-05-16
;  PRIOR APPLICATION NUMBER: 10/283,023
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: 60/335,044
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/010,943
;  PRIOR FILING DATE: 2001-12-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 320
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-11-226-701-6
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  Query Match             53.2%;  Score 1280;  DB 7;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-110;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         88 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        148 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        208 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        268 T 268
              |
Db        320 T 320
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RESULT 3
US-11-091-018-10
; Sequence 10, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-10
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  Query Match             25.1%;  Score 604.5;  DB 7;  Length 507;
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  Best Local Similarity   33.3%;  Pred. No. 6.8e-48;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db          52 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 108

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         109 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 167

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         168 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 227

Qy         241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
               ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         228 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 287

Qy         299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db         288 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 347

Qy         353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
               ::  :||||:|::   |:  |:||: ||| ||:  ||        ::::|  |  |:
Db         348 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 405

Qy         413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
               ::| :|:      |    ||    |:  ::|        |::|:|
Db         406 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 444
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RESULT 4
US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-9

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  Query Match           25.1%;  Score 604.5;  DB 7;  Length 585;
  Best Local Similarity   33.3%;  Pred. No. 8.2e-48;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db         130 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 186

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         187 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 245

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         246 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 305

Qy         241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
               ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db         306 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 365

Qy         299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                 |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db         366 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 425

Qy         353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
               ::  :||||:|::   |:  |:||: ||| ||:  ||        ::::|  |  |:
Db         426 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 483

Qy         413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
               ::| :|:      |    ||    |:  ::|        |::|:|
Db         484 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 522
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RESULT 5
US-11-091-018-6
; Sequence 6, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretarsdottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-6

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  Query Match           25.1%;  Score 604.5;  DB 7;  Length 673;
  Best Local Similarity   33.3%;  Pred. No. 9.9e-48;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy          66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
               |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db         218 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 274

Qy         122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                 | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db         275 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 333

Qy         181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
               | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db         334 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 393
```

```
Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        394 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 453

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        454 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 513

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        514 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 571

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |::|:|
Db        572 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 610


RESULT 6
US-11-091-018-8
; Sequence 8, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 687
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-8

  Query Match             25.1%;  Score 604.5;  DB 7;  Length 687;
  Best Local Similarity   33.3%;  Pred. No. 1e-47;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        232 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 288

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        289 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 347

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| |||||||||:  ||| ||  || :| : |
Db        348 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 407

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        408 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 467

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
```

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Db        468 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 527

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        528 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 585

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |::|:|
Db        586 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 624


RESULT 7
US-11-091-018-4
; Sequence 4, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 745
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-4

  Query Match             25.1%;  Score 604.5;  DB 7;  Length 745;
  Best Local Similarity   33.3%;  Pred. No. 1.1e-47;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        290 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 346

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        347 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 405

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| |||||||||:  ||| ||  || :| : |
Db        406 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 465

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        466 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 525

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        526 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 585

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        586 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 643

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
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            ::| :|:      |    ||    |:  ::|        |::|:|
Db        644 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 682


RESULT 8
US-10-492-835-12
; Sequence 12, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 748
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-492-835-12

  Query Match             25.1%;  Score 604.5;  DB 6;  Length 748;
  Best Local Similarity   33.3%;  Pred. No. 1.1e-47;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|      ::  |:| |    ||:  :    || | :    | |  |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :|||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :  ::||||:::    |  ||  :
Db        469 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 528

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |        | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        529 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 588

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        589 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |::|:|
Db        647 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 685


RESULT 9
US-10-492-835-28
; Sequence 28, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 28
;   LENGTH: 748
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-492-835-28

  Query Match             25.1%;  Score 604.5;  DB 6;  Length 748;
  Best Local Similarity   33.3%;  Pred. No. 1.1e-47;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|      ::  |:| |    ||:  :    || | :    | |  |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :|||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : :  ::||||:::    |  ||  :
Db        469 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 528

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |        | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        529 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 588

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::   |:   |:||: ||| ||:  ||         ::::|  |  |:
Db        589 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
              ::| :|:      |    ||    |:  ::|        |::|:|
Db        647 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 685


RESULT 10
US-11-091-018-2
; Sequence 2, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
;  APPLICANT: Gretarsdottir, Solveig
;  APPLICANT:  Thorleifsson, Gudmar
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
;  TITLE OF INVENTION:  METHODS OF TREATMENT
;  FILE REFERENCE: 2345.2010-016
;  CURRENT APPLICATION NUMBER: US/11/091,018
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: PCT/US03/29906
;  PRIOR FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: 10/255,120
;  PRIOR FILING DATE: 2002-09-25
;  PRIOR APPLICATION NUMBER: 10/419,723
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 10/650,120
;  PRIOR FILING DATE: 2003-08-27
;  PRIOR APPLICATION NUMBER: 10/067,514
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 09/811,352
;  PRIOR FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 809
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-091-018-2

  Query Match             25.1%;  Score 604.5;  DB 7;  Length 809;
  Best Local Similarity   33.3%;  Pred. No. 1.3e-47;
  Matches  135;  Conservative   86;  Mismatches  151;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
```

```
                |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        354 KEKKKRPMSQISGVKKLMHSSSLTNSSIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 410

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        411 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 469

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| |||||||:  ||| ||  || :| : |
Db        470 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 529

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
                ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        530 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 589

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        590 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 649

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
                ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        650 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 707

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
                ::| :|:      |    ||    |:  ::|        |::|:|
Db        708 YQSTIPQ------SPSPAPDDPEEGRQGQTEKFQFELTLEEDGES 746


RESULT 11
US-10-492-835-8
; Sequence 8, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-492-835-8

  Query Match             25.1%;  Score 603.5;  DB 6;  Length 747;
  Best Local Similarity   33.3%;  Pred. No. 1.4e-47;
  Matches  135;  Conservative   85;  Mismatches  152;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
                |:| || :|     ::  |:| |    ||:  :    || | :    |  |  |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| |||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
                ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        469 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMV 528

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        529 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 588

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
                ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        589 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
                ::| :|:      |    ||    |:  ::|        |::|:|
Db        647 YQSTIPQ------SPSPAPDDQEDGRQGQTEKFQFELTLEEDGES 685


RESULT 12
US-10-492-835-27
; Sequence 27, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-492-835-27

  Query Match             25.1%;  Score 603.5;  DB 6;  Length 747;
  Best Local Similarity   33.3%;  Pred. No. 1.4e-47;
  Matches  135;  Conservative   85;  Mismatches  152;  Indels   33;  Gaps    9;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
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Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
                | |: |  |  | | :  | |:|:  : |:| |||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
                ||||||      :|:|    :  :| |:  | : : :  ::||||:::    |  ||  :
Db        469 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMV 528

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
                |       | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        529 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 588

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
                ::  :||||:|::   |:   |:||: ||| ||:  ||        ::::|  |  |:
Db        589 RERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETWADLVHPD--AQDILDTLEDNREW 646

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESE--------EQEGDS 449
                ::| :|:      |    ||    |:  ::|        |::|:|
Db        647 YQSTIPQ------SPSPAPDDQEDGRQGQTEKFQFELTLEEDGES 685


RESULT 13
US-10-492-835-15
; Sequence 15, Application US/10492835
; Publication No. US20050289660A2
; GENERAL INFORMATION:
;  APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
;  TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
;  TITLE OF INVENTION:  OF USE
;  FILE REFERENCE: MEMORY 4 WO
;  CURRENT APPLICATION NUMBER: US/10/492,835
;  CURRENT FILING DATE:  2004-04-15
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
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;   LENGTH: 747
;   TYPE: PRT
;   ORGANISM: Murine sp.
US-10-492-835-15

  Query Match             24.7%;  Score 594.5;  DB 6;  Length 747;
  Best Local Similarity   33.4%;  Pred. No. 9.6e-47;
  Matches  131;  Conservative   84;  Mismatches  152;  Indels   25;  Gaps    8;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
              |:| || :|     ::  |:| |    ||:  :    || | :    | | |   :|
Db        293 KEKKKRPMSQISGVKKLMHSSSLTNSCIPRFGVKTEQEDVLAKE---LEDVNKWGLHVFR 349

Qy        122 FDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD 180
                | :||  :|:: | :|    |:  ||: : ||  :|: ::: ||:   ||| :||||
Db        350 IAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAAD 408

Qy        181 VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMS 240
              | |: |  |  | | :  | |:|:  : |:| ||||||||:  ||| ||  || :| : |
Db        409 VVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSS 468

Qy        241 VLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHL 298
              ||||||      :|:|    :  :| |:  | : : :  ::|||:::    |  ||  :
Db        469 VLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMV 528

Qy        299 HNKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELE 352
              |      | |::  ||  :||  : |||: || :  :: :||::|: |||:|||: |
Db        529 ETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRE 588

Qy        353 QKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQ 412
              ::  :||||:|::    :   |:||: ||| ||:  ||        ::::|  |  |:
Db        589 RERGMEISPMCDKHNAFVEKSQVGFIDYIVHPLWETWADLV--HPQAQDILDTLEDNREW 646

Qy        413 WKSLLPRQHRSRGSSGSGPDHDHAGQGTESEE 444
              ::| :|:      |    ||     |:  ::|:
Db        647 YQSTIPQ------SPSPAPDDQEEGRQGQTEK 672


RESULT 14
US-11-123-893-13
; Sequence 13, Application US/11123893
; Publication No. US20060041006A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA
;  APPLICANT:  CHO, HANNA
;  APPLICANT:  ENGLAND, BRUCE
;  APPLICANT:  GILLETTE, SAM
;  APPLICANT:  ARTIS, DEAN RICHARD
;  APPLICANT:  ZUCKERMAN, REBECCA
;  APPLICANT:  ZHANG, CHAO
;  TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
;  FILE REFERENCE: 039363-1109
;  CURRENT APPLICATION NUMBER: US/11/123,893
;  CURRENT FILING DATE:  2005-05-06
;  PRIOR APPLICATION NUMBER: 60/569,435
;  PRIOR FILING DATE: 2004-05-06
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-123-893-13

  Query Match             23.7%;  Score 570.5;  DB 7;  Length 349;
  Best Local Similarity   34.4%;  Pred. No. 5.6e-45;
  Matches  122;  Conservative   77;  Mismatches  135;  Indels   21;  Gaps    7;

Qy         99 EDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH-LFNTHGLIHHFKLDMVTLHR 157
              || | :    | |  |   :|    | :|| :|:: | :|    |:  ||: : ||
Db          4 EDVLAKE---LEDVNKWGLHVFRIAEL-SGNRPLTVIMHTIFQERDLLKTFKIPVDTLIT 59

Qy        158 FLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDH 217
                :|: ::: ||:   ||| :|||||  |: |  |  | | :  | |:|:  : |:|| |||||
Db         60 YLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTPALEAVFTDLEILAAIFASAIHDVDH 119

Qy        218 PGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQL 275
              |||:  ||| ||  || :| : |||||||      :|:|    :  :| |:  | : : :
Db        120 PGVSNQFLINTNSELALMYNDSSVLENHHLAVGFKLLQEENCDIFQNLTKKQRQSLRKMV 179

Qy        276 GSLILATDINRQNEFLTRLKAHLHNKD------LRLEDAQDRHFMLQIALKCADICNPCR 329
              ::||||:::    |  ||  :  |      | |::  ||  :||  : |||: || :
Db        180 IDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLLLDNYSDRIQVLQNMVHCADLSNPTK 239

Qy        330 IWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREW 389
              :: :||::|: |||:|||: |::  :||||:|::   |:   |:||: ||| ||:  |
Db        240 PLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCDKHNASVEKSQVGFIDYIVHPLWETW 299

Qy        390 AHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGSGPDHDHAGQGTESEE 444
              |        ::::|  |  |:  ::| :|:      |    ||    |: ::|:
Db        300 ADLVHPD--AQDILDTLEDNREWYQSTIPQ------SPSPAPDDPEEGRQGQTEK 346


RESULT 15
US-11-169-041-207
; Sequence 207, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;  TITLE OF INVENTION:  COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;  TITLE OF INVENTION:  KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 10001 NP
;  CURRENT APPLICATION NUMBER: US/11/169,041
;  CURRENT FILING DATE:  2005-06-28
;  PRIOR APPLICATION NUMBER: 60/584,405
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 527
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
;   LENGTH: 736
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-169-041-207

  Query Match             23.6%;  Score 567.5;  DB 7;  Length 736;
  Best Local Similarity   31.3%;  Pred. No. 3e-44;
  Matches  129;  Conservative   93;  Mismatches  149;  Indels   41;  Gaps    8;

Qy         66 KKKVKRLLS----FQRYFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFL 121
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Db        298 KKKKQQLMTQISGVKKLMHSSSLNNTSISRFGVNTENEDHLAKELEDLNK---WGLNIFN 354

Qy        122 FDRLTNGNSLVTLLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADV 181
                 ::   |  ::  :|    |:  |::   |   ::: ::: |||   |||::|||||
Db        355 VAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADV 414

Qy        182 TQAMHCYLKEPKLASFLTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSV 241
              |: |  |  | | :  | |:|:  : ||| ||||||||:  ||| ||  || :| : ||
Db        415 AQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 474

Qy        242 LENHHWRSTIGMLRESR--LLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLH 299
              |||||      :|:|    :  :| |:  | : : :  ::|||:::    |  ||  :
Db        475 LENHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVE 534

Qy        300 NKD------LRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQ 353
              |      | |::  ||  :|:  : |||: || :  |: :||::|: |||::||: |:
Db        535 TKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKER 594

Qy        354 KFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQW 413
              :  :||||:|::    |:   |:||: ||| ||:  ||         ::::|  |  |: :
Db        595 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPD--AQDILDTLEDNRNWY 652

Qy        414 KSLLPRQHRSRGSSGSGP----DHDHAG------------QGTESEEQEGD 448
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Db 653 QSMIPQ-------SPSPPLDEQNRDCQGLMEKFQFELTLDEEDSEGPEKEGE 697

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Job time : 18.6829 secs